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OM nucleic - nucleic search, using sw model

Run on: January 20, 2002, 23:30:41 ; Search time 1336.89 Seconds
(without alignments) 11439.150 Million cell updates/sec

Title: US-09-530-209A-1

Perfect score: 927

Sequence: 1 ATGCGACAGAGAAATCTAGA.....CTTATACACATCTTCTTAA 927

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues 2944280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmulab

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	927	100.0	927	6	A96985	A96985 Sequence 1
2	927	100.0	1179	8	ATRI131636	AJ11636 Arabidops
3	302.2	32.6	1284	6	A85057	A85057 Sequence 1
4	302.2	32.6	1284	6	NTA011892	AJ011892 Nicotiana
5	266	28.7	1650	8	ATCD2	X83370 A. thaliana
6	261.2	28.2	88356	8	AB011479	AB011479 Arabidops
7	258.2	27.9	1699	8	CRCYCD	Y10162 C. rubrum mr
8	193.4	20.9	1846	6	A85077	AJ250397 Arabidops
9	148.2	16.0	113053	6	ATP12817	AL353995 Arabidops
10	127.8	13.8	1679	6	A85058	A85058 Sequence 2
11	127.8	13.8	1679	6	NTA011893	AJ011893 Nicotiana
12	126.2	13.6	1140	8	AMA250397	AJ250397 Arabidops
13	126.2	13.6	1414	6	A85061	AJ250397 Arabidops
14	126	13.6	1487	8	AB015222	AB015222 Nicotiana
15	123.2	13.3	1788	6	A85060	A85060 Sequence 4
16	118.4	12.8	1431	6	A85059	A85059 Sequence 3
17	118.4	12.8	1431	6	NTA011894	AJ011894 Nicotiana
18	115.4	12.4	1518	8	LEA2588	AJ002588 Lycopersi
19	115.4	12.4	1532	8	LES245415	AJ245415 Lycopersi
20	111.2	12.0	1162	8	AMA250396	AJ250396 Arabidops
21	111.2	12.0	1951	8	ATCD1	X83369 A. thaliana
22	110.6	11.9	1460	8	LEA2589	AJ002589 Lycopersi
23	107	11.5	1628	8	AB008188	AB008188 Pisum sat
24	106.2	11.5	1451	8	AMA250398	AJ250398 Arabidops
25	104.2	11.2	1861	8	MSCYCPROT	X88864 M. sativa mr
26	101	10.9	1449	8	LEA2590	AJ002590 Lycopersi
27	99.8	10.8	1214	8	CRU011776	AJ011776 Chenopodi
28	93	10.0	1632	8	ATCD3	X83371 A. thaliana
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35	57.8	6.2	1141	6	AX083744	AX083744 Sequence
36	57.6	6.2	94091	8	ATP28A23	AL021961 Arabidops
37	57.6	6.2	192861	8	ATCHRIV80	AL161584 Arabidops
38	57.6	6.2	195921	8	ATCHRIV81	AL161585 Arabidops
39	55.6	6.0	91740	8	ATF19F18	AL035605 Arabidops
40	55.6	6.0	196339	8	ATCHRIV87	AL161591 Arabidops
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42	48	5.2	1215	6	AR082520	AR082520 Sequence
43	48	5.2	1215	6	AR122708	AR122708 Sequence
44	47	5.1	87581	6	AT77H20	AL162508 Arabidops
45	46.8	5.0	114505	8	F20P5	AC002062 Sequence

ALIGNMENTS

RESULT 1
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DEFINITION Sequence 1 from Patent WO922002.
ACCESSION A96985
VERSION A96985.1 GI:6780426
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 927)
AUTHORS De,A.J. and De,V.L.
TITLE A NOVEL MITOGENIC CYCLIN AND USES THEREOF
JOURNAL Patent: WO 9922002-A 1 06-MAY-1999
ALMEIDE JANICE DE (BE); VEYDER LIEVEN DE (BE)
FEATURES
source
1. 927
Location/Qualifiers
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1. 927

CDS

1. 927

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SVORMELIVLUNKRLRLAIRTPCSYIRFLRMSKCDDEPSFTLSRLOVYASTTKG
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BASE COUNT      269 a      148 c      223 g      287 t
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Query Match      100.0%; Score 927; DB 6; Length 927;
Best Local Similarity 100.0%; Pred. No. 5.5e-222;
Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 61 GGCATGATTTGTTGAGCAAACTCCGATTTGAAATTTGCAATTCAGATGGGTTTTCTCAA 120
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DB 61 GGCATGATTTGTTGAGCAAACTCCGATTTGAAATTTGCAATTCAGATGGGTTTTCTCAA 120
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OY 361 TGGATATTGACAGTTGTTGGCTGTGGCTTGTATTCATTTGACACCAAAATTTGAAGAACT 420
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DB 361 TGGATATTGACAGTTGTTGGCTGTGGCTTGTATTCATTTGACACCAAAATTTGAAGAACT 420
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DB 721 TTGCGAGAGAGTACATTTGACAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAA 780
OY 781 GAGAGAGTGAAGAGATGAGGAGAAATGATGAGAGATGATGATGATGATGATGATGATG 840
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DB 781 GAGAGAGTGAAGAGATGAGGAGAAATGATGAGAGATGATGATGATGATGATGATGATG 840

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OY 841 ACACCCATGAGGCTTTTAAAGATGCGCTGTTGTTTCAGCTTTTAAAGCCCATGATCT 900
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OY 901 TCTTCTCTTATACACATCTTCTCTTAA 927
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DB 901 TCTTCTCTTATACACATCTTCTCTTAA 927
RESULT 2
ATH131636 1179 bp mRNA PLN 24-APR-1999
LOCUS
DEFINITION
ACCESSION AJ131636.1 GI:4688614
VERSION
KEYWORDS cycd4.1 gene; D-type cyclin.
SOURCE
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1179)
de Veylder, L., De Almeida Engler, J., Bursens, S., Manevski, A.,
Lescure, B., Van Montagu, M., Engler, G. and Inze, D.
A new D-type cyclin of Arabidopsis thaliana expressed during
lateral root primordia formation
Unpublished
2 (bases 1 to 1179)
de Veylder, L.
Direct Submission
Submitted (16-DEC-1998) De Veylder L., Department of Genetics, VIB,
Laboratorium voor Genetica, K.L. Ledeganckstraat 35, Gent B-9000,
BELGIUM
FEATURES
source
location/Qualifiers
1..1179
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BASE COUNT      374 a      185 c      254 g      366 t
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Query Match      100.0%; Score 927; DB 8; Length 1179;
Best Local Similarity 100.0%; Pred. No. 5.6e-222;
Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGCGAGAGAAAATCTAGAACTGAGCTTTTATGTACAGAGAGCAACGTTGATGTAG 60
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DB 118 ATGCGAGAGAAAATCTAGAACTGAGCTTTTATGTACAGAGAGCAACGTTGATGTAG 177
OY 61 GGCATGATTTGTTGAGCAAACTCCGATTTGAAATTTGCAATTCAGATGGGTTTTCTCAA 120
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DB 178 GGCATGATTTGTTGAGCAAACTCCGATTTGAAATTTGCAATTCAGATGGGTTTTCTCAA 237
OY 121 TCGGAGAGTGAGAGATTATCATGAGATGCTGAGAGAGAGAGAGAGCATTTGCCAAGT 180
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DB 238 TCGGAGAGTGAGAGATTATCATGAGATGCTGAGAGAGAGAGAGAGCATTTGCCAAGT 297

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OY	241	GCCCTCAATTGGATTTGGAAGGCTTGTGAAGTACACCGACTTTGGACATTGTGTTTTC	300
Db	358	GCCCTCAATTGGATTTGGAAGGCTTGTGAAGTACACCGACTTTGGACATTGTGTTTTC	417
OY	301	TTACGATGAACACTCTTGATCCATTCTTATCGGTTGATGATTTGCCATGCGCAAGGT	360
Db	418	TTACGATGAACACTCTTGATCCATTCTTATCGGTTGATGATTTGCCATGCGCAAGGT	477
OY	351	TGGATATTGCGAGTTGGGCTGTGGCTGTGTTTACATTTGGCACCAGCAAAATTTGAAGAACT	420
Db	478	TGGATATTGCGAGTTGGGCTGTGGCTGTGTTTACATTTGGCACCAGCAAAATTTGAAGAACT	537
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OY	481	TCAGTCCAAAGATGAGAGCTTTTGGTGTGAACAAATTTGAATGGAGATTGAGAGCAATA	540
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OY	781	GAGAGAGTGAAGAGATAGAGGGAATGATAGAGAGTATGATGATGATGATGATGATGATGAT	840
Db	898	GAGAGAGTGAAGAGATAGAGGGAATGATAGAGAGTATGATGATGATGATGATGATGATGAT	957
OY	841	ACACCAATGGGGTTTTAGAGATATGCGGCTGTGTTTACGCTTTAAGACCATGATTTCT	900
Db	958	ACACCAATGGGGTTTTAGAGATATGCGGCTGTGTTTACGCTTTAAGACCATGATTTCT	101
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Db	1018	TCTTCTTCTTATACACATCTTCTTAA 1044	
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LOCUS	AB5057	1284 bp	DNA
DEFINITION	Sequence 1 from Patent WO9842851.	PAT	21-JAN-2000
ACCESSION	AB5057		
VERSION	AB5057.1	GI:6733798	
KEYWORDS			
SOURCE			
ORGANISM			
	Common tobacco.		
	Nicotiana tabacum		
	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheoph		
	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;		
	Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.		
REFERENCE			
AUTHORS	Murray,J.A.		
TITLE	PLANTS WITH MODIFIED GROWTH		
JOURNAL	Patent: WO 9842851-A 1 01-OCT-1998;		
FEATURES	MURRAY JAMES AUGUSTUS; HENRY (GB); UNIV CAMBRIDGE TECH (GB)		
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Best Local Similarity	68.2%	Pred. No. 2,3e-65;		
Matches 466;	Conservative 0;	Mismatches 208;	Indels 9;	Gaps 3

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OY	187	TTCATCAGAGACTTATGAAGTAGAGATTTGGATTTCAATGTGGGAAGAGACATGCCCTC	246
Db	425	TATGTGCAAGAGATGTGAAGTAGAGATTTGGATTTGATGATG---GAGAAAAGAGCCCTT	481
OY	247	AATTGGATTGGAGAGCCCTGTGAGATACACCAGTTTGGACATGTGTTTTCCTTAGACA	306
Db	482	GATTGATTTTGAAGCCCTCATATGCACATTCGATTTGGAGAGCTGATTTTGTGTG	541
OY	307	ATGACCTACTTGGATGATGATTTCTTATCGTTTCATGATTTTCCATAGTGGCAAGGTTGAT	366
Db	542	ATAAATTAATCTTGATGATGATTTTCATCTCGTATGATTTGGCAAGAAATTAACCTTGGACA	601
OY	367	TTGCACTTGTGGCTGTGCTGCTGCTGTTTATCATTTGGACGCCCAAATTTGAAGAACTGAGTT	426
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OY	487	CAAGAAATGAGACCTTTTGGTGTGAACAATTTGAATTTGAGATTTGAGCAATTAAGTCCA	546
Db	722	CAAGAAATGAGAACTTTTGGATTTAAGCACATTTGAAGTGGAAATGCAAGATTTATACACT	781
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Db	782	TACACATTCATGATATTTTATGAGAAAGATG---AATGTGATCAAAATCCCATCTCGG	838
OY	607	ACATGATATTCAGATCATTTACAGATGATGACGACCAACCAAGAGTATTCATCTTTT	666
Db	839	CGGTGATTTTGGATTCATGACATGACACATGATTAATGAATATAAGAAATTTGATTTCTTG	898
OY	667	GAGTTAGACCTTTCTGAGAACCTGCTGCTGTGGGCACTTTCTTTCTGTGAGAAATTCAG	726
Db	899	GAAATTCAGCTTCTTCAAAATTTGACAGATCAGTGCATATGCTCTTTCTCAGGGAAATACAA	958
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Db	959	GCAAAAGACATTTGATTA---GGCAATGACCTTGTCTTCATACACTTACGACAAAGGTAGA	1015
OY	787	GTGAGAGAGATAGGGCAATGAT	809
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RESULT	4
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DEFINITION	Nicotiana tabacum mRNA for cyclin D2.1 protein (CycD2.1).
ACCESSION	AJ011892
VERSION	AJ011892.1 GI:4160297
KEYWORDS	CyCD2.1 gene; cyclin D2.1 protein.
SOURCE	common tobacco.
ORGANISM	Nicotiana tabacum
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Spermatophyta:	Magnoliophyta: eudicotsyledons: core eudicots:
Asteridae:	eunasterids I: Solanales: Solanaceae: Nicotiana.
REFERENCE	1 (bases 1 to 1284)
AUTHORS	Murray,J.A.H.
TITLE	Direct Submission

JOURNAL Submitted (07-OCT-1998) Murray J.A.H., Institute of Biotechnology,
University of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REFERENCE 2 (bases 1 to 1284)
AUTHORS Sorrell,D.A., Combettes,B., Chaubet-Gillot,N., Gigot,C. and
Murray,J.A.
TITLE Distinct cyclin D genes show mitotic accumulation or constant
level of transcripts in tobacco bright yellow-2 cells
JOURNAL Plant Physiol. 119 (1), 343-352 (1999)
MEDLINE 99097070
FEATURES
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Best Local Similarity 68.2%; Pred. No. 2.3e-65;
Matches 466; Conservative 0; Mismatches 208; Indels 9; Gaps 3;
QY 127 AGTGAAGATTATTCATGAGATGTTGAGAGAGAGAGAGAGAGAGATGATGAT 186
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DB 365 AGTGAAGATTATTCATGAGATGTTGAGAGAGAGAGAGAGAGAGATGATGAT 424
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QY 187 TATATCAAGAGATTGAGAGTGGAGATTTGAATGTTGAGAGAGAGATGCCCTC 246
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DB 425 TATGTGAGAGATTGAGAGTGGAGATTTGAGATGTTGAGATGTTGAGATGTT 481
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DB 482 GATTGATTGGAGAGCTTGTGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 541
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DB 602 GTGCACTTTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 661
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QY 547 TGCCTATCATAGATATTCTCTGAGAAAGATGATTAATGATCAAGAACATCCAAAC 606
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DB 782 TACACATTCATGATTAATTTATGAGAAAGATGATGAGATGAGATGAGATGAGATGAGAT 838
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DB 899 GAATTTGATGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 958
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QY 727 AGATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
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DB 959 GCAAGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015
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QY 787 GTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 809
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RESULT 5
ATCD2
LOCUS ATCD2 1650 bp mRNA PLN 25-MAR-1998
DEFINITION A.thaliana mRNA for cyclin delta-2 (CycD2).
ACCESSION X83370
VERSION X83370.1 GI:2995131
KEYWORDS CycD2; cyclin; cyclin D2; cyclin delta-2.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1650)
Sonl,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif
Plant Cell 7 (1), 85-103 (1995)
95210930
2 (bases 1 to 1650)
Murray,J.A.H.
Direct Submission
Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
Revised by [3]
3 (bases 1 to 1650)
Murray,J.A.H.
Direct Submission
Submitted (07-JUN-1996) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
Revised by [4]
4 (bases 1 to 1650)
Murray,J.A.H.
Direct Submission
Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
On Mar 28, 1998 this sequence version replaced gi:1402895.
location/Qualifiers
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Query Match      28.7%; Score 266; DB 8; Length 1650;
Best Local Similarity 63.5%; Pred. No. 2.8e-56;
Matches 461; Conservative 0; Mismatches 250; Indels 15; Gaps 3;

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Db      1053 AGAGT 1058
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LOCUS   AB011479.1
DEFINITION
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ACCESSION
AB011479.1
VERSION
AB011479.1
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (sites)
Kaneko, T., Kotani, H., Nakamura, Y., Sato, S., Asamizu, E., Miyajima, N.,
and Tabata, S.
Structural analysis of Arabidopsis thaliana chromosome 5. V.
Sequence features of the regions of 1,381,565 bp covered by twenty
one physically assigned P1 and TAC clones
DNA Res. 5 (2), 131-145 (1998)
98344145
2 (bases 1 to 88356)
Nakamura, Y.
Direct Submission
Submitted (02-MAR-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research, 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail: ynakam@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd-graph.cgi?c=MNAS
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/netgene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://grem1n1.zo1.iastate.edu/cgi-bin/dsp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MON23 and the 3' clone is K1904.
Location/Qualifiers
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Query Match 28.2% Score 261.2; DB 8; Length 88356;
Best Local Similarity 98.9%; Pred. No. 5.7e-55;
Matches 263; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 241 GCCCTCAATTGGATTGGAGAGCTTG 266

Db 55409 GCCCTCAATTGGATTGGAGAGCTTG 55384

RESULT 7

LOCUS CRCCYD 1699 bp mRNA PLN [19-JUN-1997]

DEFINITION C. rubrum mRNA for cycline-D like protein.

ACCESSION Y10162

VERSION Y10162.1 GI:1770189

KEYWORDS cycd1 gene; cyclin-D like protein.

SOURCE red goosefoot.

ORGANISM Chenopodium rubrum

REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots: Caryophyllales; Caryophyllales; Chenopodiaceae; Chenopodium.

1 (bases 1 to 1699)

REFERENCE Renz, A.

AUTHORS Direct Submission

TITLE Submitted (18-DEC-1996) A. Renz, Lehrstuhl fuer Pflanzenphysiologie, Universitaet Bayreuth, Universitaetsstr. 30, 95447 Bayreuth, FRG

2 (bases 1 to 1699)

REFERENCE Renz, A., Fountain, M. and Beck, E.

AUTHORS Nucleotide sequence of a cDNA encoding a D-type cyclin from a photoautotrophic cell suspension culture of Chenopodium rubrum L

TITLE Plant Physiol. In press

FEATURES

Source

1..1699

Location/Qualifiers

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/db_xref="taxon:3560"

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BASE COUNT 554 a 283 c 308 g 522 t 2 others

ORIGIN

Query Match 27.9%; Score 258.2; DB 8; Length 1699;

Best Local Similarity 64.0%; Pred. No. 2.5e-54;

Matches 440; Conservative 0; Mismatches 236; Indels 9; Gaps 3;

Qy 123 GGAGAGTGGAGGAGATTATCATGAGATGCTGGGAGAGAGACACATTGGCCAGTGA 182

Db 603 GGCAATATCATAGCTGTGGCGCTTCCTGTTTCACATGAAGACAAACATTTCTGGGCTCT 662

Qy 183 TCATTACATCAAGACACTTAGAAGTGGAGAGATTGGATTGAAATGTTGAAGAAGAGATGC 242

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OY	201	TAGAAGTGGAGATTGGATTTCGAATGTGGAGAAGAGATCCCTCAATTGATTGGAA	260
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OY	321	TGCAATCTTATCGGTTTCATGATTTGGCCTAGAGGCAAGGTGGATANTGAGTTGGC	380
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OY	501	TTTGTGTGGAACAATTTGAATGAGATGAGATGAGCAATATCTCCATGCTCATACATAAG	560
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OY	561	AATATTTCTGAGAAAGATGATTAATGTGATCAAGAACCAATCCACACATGATATCTAG	620
Db	948	ATACTTTCTTCAATAATTGAGTGA---TCATGTGTGACACCTCTTGCTTGACAGCTCTCG	1004
OY	621	ATCATTTACAGTATGAGCCAGCACACCAAGATTTGACTTTTGGAGTTTAGACCTTC	680
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OY	741	CAACTCTTC 749	
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RESULT	9		
AFI2B17			
LOCUS	AFI2B17 113053 bp DNA	PLN	28-APR-2000
DEFINITION	Arabidopsis thaliana DNA chromosome 5, BAC clone F12B17 (ESSA project).		
ACCESSION	ALJ53995		
VERSION	ALJ53995.1	GI:7671438	
KEYWORDS			
SOURCE			
ORGANISM	thale cress. Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE	1 (bases 1 to 113053)		
AUTHORS	Bevan,M., Bancroft,I., Mewes,H.W., Rudd,S., Lemcke,K. and Meyer,K.F.X.		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 113053)		
AUTHORS	EU Arabidopsis sequencing,project.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-APR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mps.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bsrc.ac.uk		
COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4		

and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

Location/Qualifiers

1. 113053

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/variety="Columbia"

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447. .5927

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complement(1772. .2259)

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complement(2537. .2925)

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/number=7

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Best Local Similarity	81.8%: Pred. No. 1.2e-26;
Matches 171: Conservative 0; Mismatches 38; Indels 0; Gaps 0;	
QY 446	AGGTTGGAGATCCTCAGTTTGTGTTTGAAGGCTAAATCAGTCCAAAGAAATGAGCTTTTGG 505
Db 83236	AGGTTGGAGCTCCCATGTTTCGTTTGAGGCTAAATCAGTTCCAAAGGATGGAATCTTTGG 83295
QY 506	TGTTGACCAATTTGAAATGGAGATTGAGAGCAATATACCTCATCATATCAATATAT 565
Db 83296	TGTTGAACGTATTGAGATGGAGGTTACGCGCAGTAGCACCCGTCCTTAACGTTAGTACT 83355
QY 566	TCCGTGAGAAATGATGTAATGTGTATCAAGAACCTCACAACATGATATCTAGATCAT 625
Db 83356	TCCGTGAGTAATATCATATGCTATGATCAAGAACCCATATGCGATTTGTTACTAGATCAC 83415
QY 626	TACAAGTGTAGCCAGCACAACCAAGGT 654
Db 83416	TACAAGTGTATGACCAAGCAACAAGGT 83444
RESULT 10	
LOCUS	AB5058 1679 bp DNA 21-JAN-2000
DEFINITION	Sequence 2 from Patent WO9842851.
ACCESSION	AB5058
VERSION	AB5058.1 GI:6733799
KEYWORDS	
SOURCE	Common tobacco.
ORGANISM	Nicotiana tabacum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE	Murray,J.A. Plants with modified growth Patent: WO 9842851-A 2 01-OCT-1998;
AUTHORS	MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
JOURNAL	Location/Qualifiers
FEATURES	1. .1679 /organism="Nicotiana tabacum" /db_xref="taxon:4097"
BASE COUNT	537 a 281 c 293 g 568 t
ORIGIN	

Db 913 TTTCGACGTGTAATGCCCTGCTGTAATGGCCACATGCAATTAAGCTTCACGTTATTCATCA 972

Qy 718 GAATTCGAGAGAGTACACTTTGACAACTCTTCCTCTCTCTTCCTCACTACTCA 777

Db 973 GTTAGACCTTGTAATTCCTGTTGACTACCAAAATCAACTCTTGGGGGTTCTCAAAATTAAC 1032

Qy 778 AAGGAGAGATGAGACATAGGGGAATGATAGAGACTGATGGCTCAGACTTATGTTCA 837

Db 1033 AAGGAGAAAGTGAATTAATGCTTGTAACATATCAGAAAGTGTTCTTAACCCATTTCA 1092

Qy 838 CAACACCCAA 848

Db 1093 CACAACGCCAA 1103

RESULT 12

AMA250397

LOCUS AMA250397 1140 bp mRNA PLN 15-NOV-1999

DEFINITION Antlirrhinum majus partial mRNA for cyclin D3a (cycD3a gene).

ACCESSION AJ250397

VERSION AJ250397.1 GI:6448481

KEYWORDS cycD3a gene; cyclin D3a.

SOURCE snapdragon.

ORGANISM Antlirrhinum majus

REFERENCE 1 Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Veroniceae; Antlirrhinum.

REFERENCE 2 1 (bases 1 to 1140)

AUTHORS Gaudin,V., Lunniss,P., Fobert,P., Towers,M., Riou-Khamlichl,C., Murray,J.J., Coen,E. and Doonan,J.H.

TITLE The expression of D-cyclin genes define distinct developmental zones in Antlirrhinum apical meristems and is locally regulated by the cycloidea gene

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1140)

AUTHORS Doonan,J.H.

TITLE Direct Submission

JOURNAL Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Innes Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM

FEATURES

source

1. 1140

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/dev_stage="flower spike"

110. 1139

/gene="cycD3a"

110. >1139

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BASE COUNT 332 a 223 c 237 g 348 t

ORIGIN

Query Match 13.6%; Score 126.2; DB 8; Length 1140;

Best Local Similarity 60.2%; Pred. No. 3e-21;

Matches 209; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

Qy 233 AGAAGATGCGCCCTCAATTTGAGTGAAGCGCTGTGAAGTACACCAAGTTGGACATTG 291

Db 368 AGAGATGAGCGCTGTGAATGATGTTTAAGTCATCGGTACTATCTTTCTGCTCTC 427

Qy 292 TGTTTTTCGCTTAGCAATGACTACTTGGATGATTCCTTATCGGTTCAATGATTTGCTTAGT 351

Db	428	ACTGCGGTTCTTGCAGTTAACTATTGATGGATATTTCTATGACAACTTTCAAGTTTCAACA	487
QY	352	GGCAAAAGTTGGATATTGTCAGATTGTTGGCTGTGGCTGTTTATCATTTGGCAGCAAAAT	411
Db	488	GATTAAGCATGATGATTCATGATTGGCTGCTGTGGCTGTCTCTCTTTGGCTGCTAAAGTT	547
QY	412	GAAGAACTGAGTTCCATATGTTGATAGATCTTCAGGTTGGACATCTCAGTTTGTTT	471
Db	548	GAAGAACTCAAGTCCCTCTTCTGTTGACCTTCAGTTGAGAACTTAAGTATGTTT	607
QY	472	GAGGCTAAATAGTCCAAAGAAATGGAGCTTTGGTGTGAAACAATTTGAAATGGACATTG	531
Db	608	GAGTCAAAACCATTCATAAGAGATGACCTTTGGTGTCTTCAACACTTAATGGAAGATG	667
QY	532	AGAGCAATAACTCCATCTCTATACATAGATATTTCCTGGAAGAAAGAT	578
Db	668	AATCCAGTCACCCCAATTTTATCTTCTTGATGACATTGCTGAGAGGCT	714
RESULT	13		
LOCUS	A85061	1414 bp	DNA
DEFINITION	Sequence 5 from Patent WO9842851.		
ACCESSION	A85061		
VERSION	A85061.1	GI:6733802	
KEYWORDS			
SOURCE			
ORGANISM	Helianthus tuberosus.		
	Helianthus tuberosus		
	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheoph		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Asteridae; easterids II; Asterales; Asteraceae; Asteroideae;		
	Helianthaceae; Helianthus.		
	1 (bases 1 to 1414)		
REFERENCE			
AUTHORS	Murray,J.A.		
TITLE	PLANTS WITH MODIFIED GROWTH		
JOURNAL	Patent: WO 9842851-A 5 01-OCT-1998;		
	MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)		
FEATURES			
source	1. 1414		
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	/db_xref="taxon:4233"		
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Best Local Similarity	58.8%;	Pred. No. 3e-21;	
Matches 218;	Conservative 0;	Mismatches 153;	Indels 0; Gaps
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QY	285	ACCATTTGTTTGTTCCTTAGCAATGAACACTTGTGATTCGATCTTATATCGGTTATGATTT	344
Db	377	ACCTCTTACAGCCCAATTTTGGCCATCAATTAATCTTGATAGGTTTCTTCTTACGCTCCATTT	436
QY	345	GCGTAGTGGCAAGGTTGGATTTGCAAGTTTGGCTGGCTGGTGTATCATTTGGCAGC	404
Db	437	TCAGAAATATAACCTTGATGATTCAACTTGTGCTGTATGTTGTCTCTTTAGCTGC	496
QY	405	CAAAATTTGAAGAACTGAAGTTCCATGTTGATTTAGATCTTCAGTTGGAGATCCTCAGTT	464
Db	497	TAAATTTGAAGAACTCAAGTGCACACTTACTTACATCTTCAGATCTTCAGATAGAGCACTAAGTA	556
QY	465	TGTGTTTGAAGCTTAATTCAGTCCAAAGATGACCTTTTGGTGTGAACAAATTTGAATG	524
Db	557	CTTGTTTGAGGCTTAAAAAACAATCAAAAAATGAGACTTTTGGTGTATGTCACACTTTGAAATG	616
QY	525	GAGATTGAGACCAATTAATCTCATGCTCATACATTAAGATATTTTCTGTGAAGAAAGATGATA	584
Db	617	GAGGATGACCCAGTGAACCAATTCATATTTCTTGATTCACATTTGTAGAAGGCTTGATTT	676

OY 585 ATGATCAAG 595
Db 677 AACTGATCATG 687

RESULT 14

AB015222 1487 bp mRNA PLN 02-APR-1999
LOCUS AB015222
DEFINITION Nicotiana tabacum NtscyD3-1 mRNA, complete cds.
ACCESSION AB015222
VERSION AB015222.1 GI:4586800
KEYWORDS NtscyD3-1.
SOURCE Nicotiana tabacum cell_line:BY-2 cDNA to mRNA.
ORGANISM Nicotiana tabacum

REFERENCE
AUTHORS Eukariyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
JOURNAL Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
AUTHORS 1 (bases 1 to 1487)
REFERENCE
AUTHORS Sekine,M.
TITLE Cell cycle regulated gene
JOURNAL Published only in Database (1999) In press
AUTHORS 2 (bases 1 to 1487)
JOURNAL Sekine,M.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1998) to the DDBJ/EMBL/Genbank databases. Masami
Sekine, Nara Institute of Science and Technology, Graduate School
of Biological Sciences; Takayama 8916-5, Ikoma, Nara 630-0101,
Japan (E-mail:sekine@nibs.aist-nara.ac.jp, Tel:+81-743-72-5462,
Fax:+81-743-72-5469)
Sequence updated (19-Aug-1998).

-COMMENT
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1.1487
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EBAKVFEEKITQRMELVLSLKRPMNVYPLSEVDHITRGLKSHIMEFLKCE
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1487

polya_site /note="18 a nucleotides"

BASE COUNT 462 a 257 c 287 g 481 t
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Best local similarity 60.5%; Pred. No. 3.4e-21;

Matches 207; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

OY 233 GAAGAGATGCCCTCAATGTGATTTGGAAGCCTGTGAAGTACACCAAGTTTGACCATTTGT 292
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OY 293 GTTTTGCTTACGAAGTACTTGTGATGATTTTATCGGTTTCAATGATTTGCCTAGTG 352
Db 458 CTGCTATTCTTCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAG 517
OY 353 GCAAGGTGATATGATGATTTGTGGCTGTGCTGTTTATCATGAGCCCAAAATTTG 412
Db 518 ATTAGCTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAG 577
OY 413 AAGAACTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 472

Db 578 AAGAACTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 637
OY 473 AGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 532
Db 638 AGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 697
OY 533 GAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 574
Db 698 ATCCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 739

RESULT 15

AB5060 1788 bp DNA PAT 21-JAN-2000
LOCUS AB5060
DEFINITION Sequence 4 from Patent WO9842851.
ACCESSION AB5060
VERSION AB5060.1 GI:6733801
KEYWORDS
SOURCE Helianthus tuberosus.
ORGANISM Helianthus tuberosus

REFERENCE
AUTHORS Eukariyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Helianthus tuberosus.
JOURNAL Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
AUTHORS 1 (bases 1 to 1788)
REFERENCE
AUTHORS Murray,J.A.
TITLE PLANTS WITH MODIFIED GROWTH
JOURNAL Patent: WO 9842851-A 4 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)

FEATURES
source
1.1788
Location/Qualifiers

/organism="Helianthus tuberosus"
/db_xref="taxon:4233"
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ORIGIN

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Best local similarity 52.1%; Pred. No. 1.7e-20;
Matches 335; Conservative 0; Mismatches 175; Indels 6; Gaps 2;

OY 124 GAGAGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 183
Db 276 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 335
OY 184 GATTAATCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
Db 336 GATTAGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 392
OY 244 CTCAATTTGATTTGGAAGCCTGTGAAGTACACCAAGTTTGACCATTTGTTTGTCTTA 303
Db 393 GTTGCTGATCTTAAAGGCAAGCGTTTAAAGATTTACGATTTACGCGGTACCTTC 452
OY 304 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 363
Db 453 TCCGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 512
OY 364 ATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 423
Db 513 CCGTTGCAACTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 572
OY 424 GTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483
Db 573 ATTCTCTTATTTCTTATCTCAAGTTGAAGGTGCAAAATTAATTTTGAAGCGGAATA 632
OY 484 GTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 543
Db 633 ATCCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 692
OY 544 CCATGCTCATATACATATTTCTGAGAAAGATGATGATGATGATGATGATGATGATG 603
Db 693 CCGTTAGCTTAAATGCGCTTCTTTTGACAAATATGATGATGATGATGATGATGATG 752


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OY 604 AACACATTGATATCTAGATCATTTACAGTGAATAGCCAGCACCAAGCATTTGACTTT 663
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Db 753 TTC--CTATCTCAAGGCAACACAATTAATCTCTCAATATTCAGAAAGCTAGTTTA 809
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OY 664 TTGGAGTTTAGACCTTCTGAAGCTGCTGCTGCTGCGACCTTCTGTTCTTGAGAAATTG 723
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Db 810 CTTGAGTATTTGGCCATCATGTATGTGCTGCTGCAACAATACTTTGTGACAGCAAGTGATCTT 869
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OY 724 CAGAGGTACACTTTGACACCTCT 747
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Db 870 TCTAAATTCTCACTTATCATGCT 893
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Job time: 2930 sec

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N. tabacum CYCD3;2;
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Arabidopsis thaliana
Arabidopsis thaliana
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Oligonucleotide D1
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Oligonucleotide D2
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Oligonucleotide D2
Oligonucleotide D1
Soybean cyclin delta
Soybean cyclin delta
Wheat cyclin delta
Corn cyclin delta
Arabidopsis thaliana
Arabidopsis thaliana
Maize cyclin D Zmc0
Arabidopsis thaliana
Arabidopsis thaliana
Generic human cyclin
Human cyclin E2 am
Generic mouse cyclin
Mouse cyclin E2 am
Enterococcus faecalis
Oligonucleotide D1
EST clone J635; H

growth inhibitor;
differentiation;
; ds.

XX This sequence encodes the mitogenic cyclin, CYCD4, of the invention.
CC The DNA sequence, vectors containing it, protein encoded by it, or
CC antibodies recognising the protein can be used for modulating plant cell
CC cycle, plant cell division and/or growth, for influencing the activity of
CC mitogenic cyclin in a plant cell, as positive or negative regulator of
CC cell proliferation, for modifying the growth inhibition caused by
CC environmental stress conditions, or for use in a screening method for the
CC identification of inhibitors or activators of cell cycle proteins. A
CC compound which is an activator or inhibitor of the mitogenic cyclin can
CC be used as a growth regulator and/or herbicide. The proteins can also be
CC used to influence cell division progression in yeast, mammals and
CC insects.

XX
XX
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Query Match 100.0%; Score 927; DB 20; Length 927;
Best Local Similarity 100.0%; Pred. No. 9.8e-253;

Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GGCATGATTGTTGACGAAACTCCGATTGAAATTCGATTCCCTCAGATGGGTTTCTCAA 120
DB 61 ggcattgattgtgacgaaactccgattgaaatttcgattccctcagatgggtttctctcaa 120
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DB 421 gaagtccaatgttgatagatcttcaggtttgagatcccaagtttgttggggctaaaa 480
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DB 481 tcagtccaaagaaatgagagctttgtgtgaacaaatgaatgagattgagagaata 540
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DB 541 acttcattgctcatatcagatatttcccgagagaaatgataaagtatcagaagacca 600
QY 601 TCCAAACACATTTGATCTGATCATTCATTAAGATAGCCAGACCAACCAAGATATTGAC 660
DB 601 tccaaacacatltgatctgatcatcattacaagatagccagacacacaaagtattgac 660
QY 661 TTTTGTGACTTTAGACCTTCTGAAGCTGCTGCTGTGGACACTTTCTGTTTGTGAGAA 720
DB 661 ttttgtgactttagaccttctgaagctgctgctgtggacactttctgttttgcagaa 720
QY 721 TTGCAAGAGTACACTTTTGACAACTCTTCTCTCTCTCTTTTTCACACTACTTCAAAAG 780
DB 721 ttgcagagagtlacactlttgacaaactctctctctctcttcttctcactactcaaaag 780

QY 781 GAGACAGTGAAGACAGATAGGGAATGATGAGAGTGAAGGCTCAGACTTATGTTCAAA 840
DB 781 gaaagagtgaaagaagatagggaaatgatatagagatgagtgctcagacttatgttcaaa 840
QY 841 ACACCCCAATGGGTTTAAAGATATGCGCTGTGTTTCACTTTAAGACCATGATTCCT 900
DB 841 acaccccaatgggtttaaagatattgctgttcttcaacttttaagaccatgatctct 900
QY 901 TCTTCTTATACATCTTCTTAA 927
DB 901 tcttcttatacacatcttcttaa 927

RESULT 2

AAC48940
ID AAC48940 standard; DNA; 1287 Bp.

XX AAC48940;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 59332.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

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PR 01-APR-1999; 99US-0127462.

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PR 16-APR-1999; 99US-0129845.

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PR 21-APR-1999; 99US-0130449.

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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 99.7%; Score 923.8; DB 21; Length 1287;
Best Local Similarity 99.8%; Pred. No. 9e-252;
Matches 925; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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Query Match 99.3%; Score 920.6; DB 21; Length 1290;
Best Local Similarity 99.6%; Pred. No. 7.3e-251;
Matches 923; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db	544	tttaagaatgaactactcttggatcgactcttcaatcggttcaatgaattcttgcttagtggcaaggt	603
OY	361	TGGATATTGCAAGTTGTTGGCTGTGGCTTGGTTATTCATTTGGCAGCAGCAAAATTTGAAGAACCT	420
Db	604	tggatattgcaagttgttggcgtgtggctgtgtttatcatattggcagccaaatattgaagaact	663
OY	421	GAAGTTCCAAATGTTGATAGATCTCTCAGGTTGGAGATCCTCAGTTTGTGTTGAAGCTTAA	480
Db	664	gaagttccaatgttgatagactcttcaggttggagatcctcagtttcttgtttgggtctaa	723
OY	481	TCAGTCCAAAGAAATGGAGACCTTTTGCTGTGAACAAATTGAATGGAGATTGAGAGCAATA	540
Db	724	tcaagtccaagaataggagcttcttggttgltgaacagattgaatggagattgagaacata	783
OY	541	ACTCCATGCTCATACATAAGACTATTTCTCGAGAAAGATGAGTAAATGTGATCAAGAACCA	600
Db	784	actccatgtcatatacataagaatcttccctgagaagaatgataatgltgatcaagaacca	843
OY	601	TCCAAACACATTGATATCTAGATCTATTACAAAGTGATGCCAGCAACAACAAAGGATATTGAC	660
Db	844	tccaacacattgatatacttagatcattacaagtatagatagccagacaacaaagttatggac	903
OY	661	TTTTTGGAGTTTAGACCTTCGTGAAGCTGCGTGCAGCTGTGCACCTTCTGTCTTGAGANA	720
Db	904	tttttggagtttagaaccttcaggagtttgcgcgcgtgtggcacttcttcttctgaga	963
OY	721	TTGAGAGAGATACCTTTTGACAACTCTTCCTCTCCCTCTTTTTCACATCTTCAAAAG	780
Db	964	ttgcagagagtaaaccttggacaactcttccctctccctcttctccactactctaaag	1022
OY	781	GAGAGAGTGAGAGATATGAGGGAATGATAGAGAGTATGGCTCAACATTATGTTACAA	840
Db	1024	gagagagtgagagaaagataagggaatgatagagatgattgcttcagactatattacaa	1083
OY	841	ACACCCAAATGGGGTTTATAGAAGTATCGGCTGTGTTTGACGTTTAAAGCCATGATTCCT	900
Db	1084	acacccaatgggggtttagaagaatctcgctctgttcttcaagctttaagaaccaatgatct	1143
OY	901	TCTTCTCTTATACACATCTTTCTTAA	927
Db	1144	tcttctcttatacacatcttctttaa	1170
RESULT 4			
AAV33884	AAV33884 standard; cDNA to mRNA; 1284 BP.		
AC	AAV33884;		
XX	25-JAN-1999 (first entry)		
DT	N. tabacum CYCD2;1 gene.		
XX			
KM	D-type cyclin; growth; plant; cell-division control; phosphorylation;		
KM	CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;		
KM	root development; ds.		
XX	Nicotiana tabacum.		
OS			
XX	MO9842851-AL.		
PN			
XX	01-OCT-1998.		
PD			
XX	24-MAR-1998; 98MO-EP01701.		
PF			
XX	26-MAR-1997; 97EP-0302096.		
PR			
XX	(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.		
PA			
XX	Murray JAH;		
XX	PI		

[illegible]

[illegible]

RESULT 10

ID AAV33885 standard; cDNA to mRNA; 1679 BP.

AC AAV33885;

DT 25-JAN-1999 (first entry)

DE N. tabacum CYCD3;1 gene.

KW D-type cyclin; growth; plant; cell-division control; phosphorylation;

KW root development; ds.

OS *Nicotiana tabacum.*

PN W09842851-A1.

PD 01-OCT-1998.

PF 24-MAR-1998; 98WO-EP01701.

PR 26-MAR-1997; 97EP-0302096.

PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

PI Murray JAH;

DR WPI; 1998-532012/45.

PT Regulating growth and structure of plants by modulating protein that

PT chimeric genes and transformed cells and plants, used to alter

XX XX

PS Claim 14; p54; 75pp; English.

CC This sequence represents the CYCD3:1 cDNA from *Nicotiana tabacum* which
CC encodes a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, *Chrysanthemum*, rose, tulip, etc.

Sequence 1679 BP; 537 A; 281 C; 293 G; 568 T; 0 other;

Query Match	13.88	Score 127.8	DB 19	Length 1679
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Matches 309; Conservative 0; Mismatches 302; Indels 0; Gaps 0;

Oy 238 GATGCCCTCAATTGGATTGGAAGCGCTGTGAACTACACCAGTTTGGACCATTGTCTTT 297
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Db 493 gattctgtvgaatgqatttaaaagtqaatgqtatatatgqtlctcvtctttagactgc 552

OY	298	TGCTTACCATTGAACTACCTGGATGCGATCTTCTTAATGGCTTCAATGATTTGCTCCTAGTGGCAAA	357
OY	298		357
Db	553	gttttagccataaataacttacttgcagaagttcttgcactagctctcattatccagaagaataa	612
OY	358	GGTTGGATATTTGAGAGTTGTGGCGCTGGCTTTGTTATATCTTGGCGCCCAAAATTTGAAGAA	417
OY	358		417
Db	613	ccgtgagatgattcaactctgctcgtctgttacttgccttctttagcgcgtccaaagtttgaagaa	672
OY	418	ACTGAAGTTCCAATGTTGATAGATGTCCTTACAGGTTTGGAGATCCTCACTTTGTGTTGAGGCT	477
OY	418		477
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Db	853	cactgggaattctctagaagatgltgaaaaatctcctcctctcattatgctgcatgtlaga	912
OY	658	GACTTTTGGAGTTTAACCTTCTGGAAGCGTGCCTGCTGCTGGGCACTTTGTTCTTCTGGA	717
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OY	718	GAAATTGCGAGAGATACACTTTTGACAACCTCTTCTCTCCCTTTTTCGACTACTTCAA	777
OY	718		777
Db	973	gttgaagccttgtaattctctgttgaactaccaaaatacaactctcttggggttctccaataatcac	1032
OY	778	AAGGAGACAGTGAAGAGATATGGGAAATGATATAGAGAGTGATGGCTCAGACTTATGTTCA	837
OY	778		837
Db	1033	aaggaagaangtaataatgcttcttgaactcatacagaaagtgtgtcttaagaccatttca	1092
OY	838	CAACACCCCA	848
OY	838		848
Db	1093	cacaacgcgca	1103

RESULT 11

ID AAV33888 standard; cDNA to mRNA; 1414 BP.

AAV33888;

DT 25-JAN-1999 (first entry)

DE H. tuberosus CYCD3;1 gene.

KW D-type cyclin; growth; plant; cell-division control; phosphorylation;

KW root development; ds.

05 Helianthus tuberosus.

PN W09842851-A1.

PD 01-OCT-1998.

PF 24-MAR-1998; 98WO-EP01701.

PR 26-MAR-1997; 97EP-0302096.

PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

PI, Murray JAH,

DR WPI; 1998-532012/45.

PT Regulating growth and structure of plants by modulating protein that
PT controls cell division - specifically a D-type cyclin, and related

PT chimeric genes and transformed cells and plants, used to alter
PT growth rate, flowering, seed production etc.
XX Claim 14; p58; 75pp; English.
XX
XX This sequence represents the CYCD3:1 cDNA from Helianthus tuberosus which
CC encodes a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.
XX
XX
SQ Sequence 1414 BP; 449 A; 276 C; 248 G; 441 T; 0 other;

Query Match 13.6%; Score 126.2; DB 19; Length 1414;
Best Local Similarity 58.8%; Pred. No. 7.7e-26;
Matches 218; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 225 TGTGTGAAGAGAGATGCCCTCAATTGGATTGGAGGCTTGTGAAGTACACCAGTTGG 284
DB 317 Tgcgtctgtaagaagcgcgtgagatgagatcccttaaggtcaaaagttgtatgattcac 376
QY 285 ACCATTGTGTTTTGCTTCATGACATGACTTGGATTCATTCCTATTCGCTTCATGATT 344
DB 377 acctcttaagcattttagccatcaattatcttgtagtcttcttcagccctcattt 436
QY 345 GCCCTAGTGCCTCAAGGTTGGATTTGCAAGTTGGCTGTGGCTTGTTCATTTGACAGC 404
DB 437 tcaagaagataaaccttgatgattcaacttgctgtgtagtgcctcctttagctgc 496
QY 405 CAAATATGAGAACTGATGATGCTTCATGATGATGATGATGATGATGATGATGATGAT 464
DB 497 taagttgtaagaagacccaagtcgactcttaagatcttcaagtagaagaactaagta 556
QY 465 TGTGTTGAGGCTAAATCAATCCAAAGAAATGAGCTTTGTGTTGTAACAATTTGAATG 524
DB 557 ctgttggtggtctaaacatacaaaaatgagccttggtagtgcacttgaacttgaatg 616
QY 525 GAGATTGACATATATACATGCTGCTACATACATATGATTTTCTTGAAGAAATGAGTAA 584
DB 617 gaggatgaaccacagtgacacacatctcattcttgatcaacatgtgaagaagcttgatt 676
QY 585 ATGTGATCAAG 595
DB 677 aactgatactg 687

RESULT 12
AAV33887
ID AAV33887 standard; cDNA to mRNA; 1788 BP.
XX
XX AAV33887;
XX
XX 25-JAN-1999 (first entry)
XX
XX H.tuberosus CYCD1:1 gene.
XX
XX D-type cyclin; growth; plant; cell-division control; phosphorylation;
KM CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
KM root development; ds.
XX
XX Helianthus tuberosus.
XX
XX W09842851-A1.
XX
XX PD 01-OCT-1998.

PF 24-MAR-1998; 98MO-EP01701.
XX
XX 26-MAR-1997; 97EP-0302096.
XX
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX Murray JAH;
XX
XX WPI; 1998-532012/45.
XX
XX
XX Regulating growth and structure of plants by modulating protein that
PT controls cell division - specifically a D-type cyclin, and related
PT chimeric genes and transformed cells and plants, used to alter
PT growth rate, flowering, seed production etc.
XX
XX Claim 14; p56-57; 75pp; English.
XX
XX This sequence represents the CYCD1:1 cDNA from Helianthus tuberosus which
CC encodes a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.
XX
XX
SQ Sequence 1788 BP; 511 A; 386 C; 387 G; 504 T; 0 other;

Query Match 13.3%; Score 123.2; DB 19; Length 1788;
Best Local Similarity 52.1%; Pred. No. 6e-25;
Matches 325; Conservative 0; Mismatches 293; Indels 6; Gaps 2;

QY 124 GAGAGTGAGAGATTTTCATGAGATGGAGAGAGAGAGAGATTTGCCAATGAT 183
DB 276 gacttgagatcgatcgacgcgaggttataagacagagaaagtcgtccagaatc 335
QY 184 GATTATACACAGAGACTTGTGAAGTGGAGATTGGATTGAATGTTGCAAGAAAGATGCC 243
DB 336 gattagctgagagatlltaalcogcaagtcctgat---gcttcgtcagagaagaatcg 392
QY 244 CTCATTTGCAATTTTGAAGCTTGTGAAGTACACCACTTTGGACCATTTGTTTCTTA 303
DB 393 gtgccttgagatcccttaaggtgcaacggttlltaagatlltaacccgttgacggtcacc 452
QY 304 GCAATGACTACTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 363
DB 453 tccgttaactatctgagatctgattcatctatctgcgtggtcctccggtgcaaatgggtg 512
QY 424 GTTCCATGTTGATATATCTTCAAGTTTGAAGATCCCACTGTTTGTGTAAGCTTAATCA 483
DB 573 attcctctatcttcttgatctccaggttggaaggtgcaaaatatacttgcagccgaaaaa 632
QY 484 GTCGCAAGAAATGAGCTTTTGTGTAACAATTTGAATGAGATTGGAGCAATTAAT 543
DB 633 atccgaagaatgaggttctctgcttaaggttggatggagactaagatccgttaca 692
QY 544 CCATGCTCATATACATATGATTTTCTGAGAAGATGATTAATGTTGATCAAGAACCATCC 603
DB 693 ccgtttagctttagtgccttcttgcacaataatgatccatctggaatgtatagaggt 752
QY 604 AACACATGATATCTAGATCAATTAACAAGTGAATGCCAGCAACAACAAGATTTGACTTT 663
DB 753 ttc---ctatctcaagggcaacaacaattatctctcaataatactcaagaagcttla 809
QY 664 TTGGAATTTAGACCTTCTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723

Db 810 cttagactctgagccatcatgtatctgcgcgtgcaacaatactcttgacgagcaagtgcctc 8659

Qy 724 CAGAGACTACACTTTGGACCAACTCT 747

Db 870 tctaaattctcattcatcaatgct 893

RESULT	13
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ID	AAV33886 standard; cDNA to mRNA; 1431 BP

Db	563	tgatctcgtactcgcgtctccgaagaataagcccttgatgatactctgctctgcgc	6222
OY	387	TTGTTTATCATTGGCAGCCAAATTTGAAGAACTGAAAGTTCATGTTGATAGATCTTCA	446
Db	623	tgtcttctctctcgtcctaagaatggaagaccacccctccctctctcttagaccctca	6822
OY	447	GTTTGGAAGATCCTCAGTTGTTGTTGGAGGCTAAATTCAGTCCAAAGATGAGCGCTTTTGGT	506
Db	683	agtcgctgattccaagatttgcgtcttgaggccaagactatccaagaaatggaactctcgt	742
OY	507	GTTGAAACAATTTGAATAGGATGAGAGCAATTAATCCATGCATACATACATTAAGATATTT	566
Db	743	gtctcccccctcttaagtggaaataagaaatccaatgacccaactatcttctcatgatcatat	802
OY	567	CCTGAGAA	574
Db	803	catggaga	810

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RESULT 14
AAC40202
ID AAC40202 standard; DNA; 1311 BP

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PR 27-JUL-1999; 99US-0145913.
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PR 31-AUG-1999; 99US-0151438.
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PR 10-SEP-1999; 99US-0153070.
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PR 24-SEP-1999; 99US-0155659.
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PR 04-OCT-1999; 99US-0157117.
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PR 28-OCT-1999; 99US-0161920.

Search completed: January 21, 2002, 00:21:58
Job time: 2927 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2002, 23:31:06 ; Search time 43.26 Seconds
(without alignments)
4853.100 Million cell updates/sec

Title: US-09-530-209a-1

Perfect score: 927
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	43.6	4.7	1212	4	US-09-222-851-18
5	40.6	4.4	7218	1	US-08-232-463-14
6	35.8	3.9	1325	1	US-08-306-691B-51
7	35.8	3.9	4221	1	US-07-947-120-7
8	35.8	3.9	4221	1	US-08-472-893A-7
9	35.8	3.9	4221	2	US-08-947-492-7
10	35.8	3.9	4244	3	US-08-460-694-1
11	35.8	3.9	4244	3	US-08-460-744-1
12	35.8	3.9	4244	3	US-07-667-711B-1
13	35.8	3.9	4453	1	US-08-770-761A-4
14	35.8	3.9	4540	1	US-08-770-761A-6
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44	31.8	3.4	4072	4	US-09-245-041-16	Sequence 16, Appl1
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ALIGNMENTS

RESULT 1

US-09-092-770-8

Sequence 8, Application US/09092770

Patent No. 5973119

GENERAL INFORMATION:

APPLICANT: Coats, Steven R.

APPLICANT: Bass, Michael B.

APPLICANT: Robinson, Murray O.

TITLE OF INVENTION: No. 5973119el Cyclin E genes and proteins

FILE REFERENCE: A-524

CURRENT APPLICATION NUMBER: US/09/092,770

CURRENT FILING DATE: 1997-06-05

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 8

LENGTH: 1215

TYPE: DNA

ORGANISM: Human

US-09-092-770-8

Query Match 5.2%; Score 48; DB 2; Length 1215;

Best Local Similarity 32.5%; Pred. No. 0.00019;

Matches 110; Conservative 60; Mismatches 159; Indels 9; Gaps 2;

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QY	292	TGTTTGGCTTGAACATGATGATGATGATGATGATGATGATGATGATGATGATG	351
DB	484	acntlytlaytngcncargayltlytlygymntlyatyltnacncaraargaytha	543
QY	352	GGCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	411
DB	544	aaraa-----yaltyncaarylnathgnathacwshnlytlyathgcnshnary	597
QY	412	GAGGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	471
DB	598	gargarathtlaygcncaarylncargartly---gcnlaytnacngayyngncty	654
QY	472	GAGGTAATCATGCTCAAGATGAGCTTTGCTTGAACAAATTGAATGAGATG	531
DB	655	wngargargayathlytmgnatlgargylnachabthynaagcnylnaarggargy	714
QY	532	AGACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	569
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Db 712 tgyccnglnacnglnathtwntlgyltnaaylntlyt 749

RESULT 5

US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHERFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232.463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935.313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-fls
US-08-232-463-14

Query Match 4.4%; Score 40.6; DB 1; Length 7218;
Best Local Similarity 6.0%; Pred. No. 0.055;
Matches 19; Conservative 166; Mismatches 130; Indels 0; Gaps 0;

OY 3 GGCAGAGAAATCTAGAACTGCTTTTATGTACAGAGACGAGTGTGATGAGG 62
Db 1339 RRR 1280
OY 63 CATGATTTGTGAGCAACCCGATTCGAATTTTCGATCTCTCAGATGGTTTCTCAATC 122
Db 1279 RRR 1220
OY 123 GGAGAGTGGAGATATCATGAGATGCTGAGAGAGACACATTTGCCAAGTGA 182
Db 1219 RRR 1160

OY 183 TGATTACATCAGAGACTTAGAAGTGCAGATTGCGATTGCAATGTGGAAGAAGATGC 242
Db 1159 RRR 1100
OY 243 CCTCAATGATTTGGAGGCTTGTGAAGTACACCGATTGGACCATTTGTTTTCCTT 302
Db 1099 RRR 1040
OY 303 ACCAATGAACACTT 317
Db 1039 ACCTCGAATTAAT 1025

RESULT 6

US-08-306-691B-51
Sequence 51, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306.691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-306-691B-51

Query Match 3.9%; Score 35.8; DB 1; Length 1325;
Best Local Similarity 48.7%; Pred. No. 0.6;
Matches 165; Conservative 0; Mismatches 162; Indels 12; Gaps 2;

OY 241 GCCCTCAATTTGGAGGCTTGTGAAGTACACAGTTTGACCATTTGCTTTTCG 300
Db 322 GTGCCACCTGATGCTGCGAGTCTCGAGAGACAGAGTGCAGAGAGGCTTCCCG 381
OY 301 TTAGCAATGAACACTTGTGATCGATTCTTATCGTTCAATGATTTGCTAGTGGCAAGGT 360
Db 382 CTGGCCATGAACACTGCGACGCTTCCTGCTGAGAGCCCTG-----AAAAAG 432
OY 361 TGCAATATGACAGTTGCTGCTGTGCTTGTATTCATTTGCGACCAAAATGAAGAACT 420

Query Match	3.9%	Score 35.8;	DB 1;	Length 4221;
Best Local Similarity	48.7%;	Pred. No. 1;		
Matches 165;	Conservative	0;	Mismatches 162;	Indels 12;
				Gaps 2;

QY 241 GCTCAATTGGATTGTGGAGGCGTTGGAAAGTACACAGTTTGGACATTGTCTTTTTC 300

Db 319 GTCCCACTCGATGCTGGAGGCTGTGGAGAACAGAAATGGACGAGGAGGAGTCTTCCG 378

QY 301 TTACCAATGAACACTCTGGATCGATTTCTATTCGGTTATGATTGGCTAATGGCAAGT 360

Db 379 CTGGCCATGAACCTACCTCGACCGCTTCTCTGCTGCTGAGGCCGTG -----AAAAG 429

QY 361 TGGATATTGCAGTGTGGCTGTGGCTTGTATTCATTGGCAGCCAAAATTGAGAACT 420

Db 430 AGCCGCGTGCAGTCTGGGGGCCACTTGCATGTTCTGGCCCTAGATGAAGGAGAC- 488

QY 421 GAATTCCAATGTGATAGATCTTCAGCTTGGAGATCTCAATTGTGTTGAGGCTAAA 480

Db 489 --CATCCCCCTGACGGCCGAGAAAGCTGTGCATCTACACCGACAACCTCATCCGCCGAG 546

QY 481 TCAATCCAAAGAAATGGAGCTTTTGGTGTGAACAAATTTGAATATGGAAATGAGAGCAATA 540

Db 547 GAGTGTCTGCAAAATGGAGCTCTCTGTGTGAACAAAGCTCAAGTGAAGAACTGGCCGCAATG 606

QY 541 ACTCCATGCTCATACATAGAATATTCTCTGGAAGAATG 579

Db 607 ACCCCGACATTTTCATTGAACACTTCTCTCCAAATG 645

RESULT 9

```

US-08-947-492-7
Sequence 7, Application US/08947492
Patent No. 6127118
GENERAL INFORMATION:
APPLICANT: Wecker, Timothy C.
TITLE OF INVENTION: BCL-1 Locus Nucleic Acid Probes and
TITLE OF INVENTION: Assay Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: Steuatt Street Tower, 18th Fl., One Market
STREET: Plaza
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,492
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,893
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-210-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 142..1026
US-08-947-492-7

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Query Match	3.9%	Score 35.8;	DB 3;	Length 4221;
Best Local Similarity	48.7%;	Pred. No. 1;		
Matches 165;	Conservative 0;	Mismatches 162;	Indels 12;	Gaps 2

Qy	241	GCCTCAATGATTTTGGAAAGCCTGGGAGAGTACACAGTTTGGACATTGTGTTTTTG	300
Db	319	GTCCGCACCTGGAGTCGGAGAGTCTGGAGGAACAGAAAGTCGAGGAGAGGTCTTCCG	378
Qy	301	TTAGCAATGAACTACTTGGATCGATTCATACGGTTCATGATTTGCTAGTGGCAAAAGT	360
Db	379	CTGGCCATGAACTACCTGGAGCCGTTCTCTGTGCTGGAGCCCGT-----AAAAAG	429
Qy	361	TGGATATTGCAATTGTTGGCTGTGGCTTGTATTATTCATGGCAGCCAAAAATTGAAGAACT	420
Db	430	AGCGCGCTGACAGTCTGGGGGCCACATTGCATGTTCTGGGCTCTAAGATGAAGGAGAC-	488
Qy	421	GAAGTTCCAATGTTGATGATCTTCAGGTTGGAGACTCTCAGTTGTGTTGAAGCTAAA	480
Db	489	--CATCCCCCTGAGCGCCGAGAACTGTGCATTCACCGCAACCTCCATCCGGCCGAG	546
Qy	481	TCAGTCCAAAGATGAGAGCTTTTGGTGTGAACAAATGGAATGGAGATTGAGAGCATATA	540
Db	547	GAGCTGCTGCAAAATGGAGAGCTCTCTCGTGAACAGCTCAAGTGAACCTGGCGCAATG	606
Qy	541	ACTCATGCTCATACATAGATATTTCCTGGAGAAGTG	579
Db	607	ACCCGCGACGATTCATTTGAACACTCTCCTCTCCAAATG	645

RESULT 10

US-08-460-694-1
Sequence 1-1, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC..
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConachy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609,4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 148..1035
US-08-460-694-1

Query Match 3.9%; Score 35.8; DB 1; Length 4540;
 Best Local Similarity 48.7%; Pred. No. 1.1;
 Matches 165; Conservative 0; Mismatches 162; Indels 12; Gaps 2;

OY 241 GCCCCTCAATGGATTGGAGGCTTGTAAGTACACAGTTTGGACCATTTGTTTTC 300
 DB 2533 GTCCGACCTGGATGCTGGAGGCTGCGAGACAGAAATGGAGAGAGAGCTTCCCG 2592
 OY 301 TTAGCAATGAACTACTTGGATGATCTTATCGTTTCATGATTTGGCTTAAAGGT 360
 DB 2593 CTGGCCATGAATTAAGTGGAGCCGCTTCTGCTGGAGACCCGCTG-----AAAAG 2643
 OY 361 TGGATATTGCACTTGTGGCTGTGGCTTTATCATTTGGCAGCCAAAATTGAAGAACT 420
 DB 2644 ACCCGCTGCACTGTGGGCGCCACTTCATGTCGTGCTTAAGATGAAGAGAGAC- 2702
 OY 421 GAAGTTCCAAATGTTAGATCTTCAGTTTGGAGATCTCAGTTTGTGTTGAGGCTTAA 480
 DB 2703 --CATCCCTTACGCGCCGAGAAAGCTGTGCATCTACCGACAACCTCCATCCGCGCGAG 2760
 OY 481 TCAGTCCAAAGATGAGCTTTTGTGTGAACAAATGAAATGAGATTGAGAGCAATA 540
 DB 2761 GAGCTGCTCAATGAGAGCTGCTCGTGTGAACAAAGCTCAAGTGAAGAACTGGCGCAATG 2820
 OY 541 ACTCCATGCTCATACATAAGATATTTCCTGAGAAAGATG 579
 DB 2821 ACCCGCAGCAATTCATTAAGACACTTCCTCCAAAATG 2859

RESULT 15

US-08-770-761A-1
 ; Sequence 1, Application US/08770761A
 ; Patent No. 5814503

GENERAL INFORMATION:

APPLICANT: Kovacevic, Steven

APPLICANT: Rao, Ramachandra N.

TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company

STREET: Lilly Corporate Center/Patent Division

CITY: Indianapolis

STATE: IN

COUNTRY: USA

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,761A

FILING DATE: 19-DEC-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Gaylo, Paul J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-10136

TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-376-0756

TELEFAX: 317-277-1917

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4621 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-770-761A-1

Query Match 3.9%; Score 35.8; DB 1; Length 4621;
 Best Local Similarity 48.7%; Pred. No. 1.1;
 Matches 165; Conservative 0; Mismatches 162; Indels 12; Gaps 2;

OY 241 GCCCCTCAATGGATTGGAGGCTTGTAAGTACACAGTTTGGACCATTTGTTTTC 300
 DB 2484 GTCCGACCTGGATGCTGGAGGCTGCGAGACAGAAATGGAGAGAGAGCTTCCCG 2543
 OY 301 TTAGCAATGAACTACTTGGATGATCTTATCGTTTCATGATTTGGCTTAAAGGT 360
 DB 2544 CTGGCCATGAATTAAGTGGAGCCGCTTCTGCTGGAGACCCGCTG-----AAAAG 2594
 OY 361 TGGATATTGCACTTGTGGCTGTGGCTTTATCATTTGGCAGCCAAAATTGAAGAACT 420
 DB 2595 ACCCGCTGCACTGTGGGCGCCACTTCATGTCGTGCTTAAGATGAAGAGAGAC- 2653
 OY 421 GAAGTTCCAAATGTTAGATCTTCAGTTTGGAGATCTCAGTTTGTGTTGAGGCTTAA 480
 DB 2654 --CATCCCTTACGCGCCGAGAAAGCTGTGCATCTACCGACAACCTCCATCCGCGCGAG 2711
 OY 481 TCAGTCCAAAGATGAGCTTTTGTGTGAACAAATGAAATGAGATTGAGAGCAATA 540
 DB 2712 GAGCTGCTCAATGAGAGCTGCTCGTGTGAACAAAGCTCAAGTGAAGAACTGGCGCAATG 2771
 OY 541 ACTCCATGCTCATACATAAGATATTTCCTGAGAAAGATG 579
 DB 2772 ACCCGCAGCAATTCATTAAGACACTTCCTCCAAAATG 2810

Search completed: January 21, 2002, 00:20:01
 Job time: 2935 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2002, 22:59:31 ; Search time 1163.67 Seconds

(without alignments)
8560.276 Million cell updates/sec

Title: US-09-530-209A-1

Perfect score: 927
Sequence: 1 ATGCGACGAGGAAATCTAGA.....CTTATACATCTTCTTA 927

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: qd_est1:*
11: qd_est2:*
12: qd_hic:*
13: qd_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_hiv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264.6	28.5	673	11	BG129531 EST47517
2	202.4	21.8	631	10	AM507921 s147a06.y
3	169.2	18.3	512	10	AT1728767 BNLGH1115
4	163.4	17.6	790	11	BI306295 NL_4_B12
5	153	16.5	562	10	AT1728683 BNLGH1113
6	149.2	16.1	381	13	CNS00055 Arabidops
7	149.2	16.1	621	10	BE442681 BNLGH1101_A
8	123.6	13.3	478	10	BE642779 Cri12_6_P2
9	116	12.5	813	10	AV527915 AV527915
10	111.8	12.1	596	10	AM042725 ST24F07_P
11	111.6	12.0	498	11	BG726093 sae06h09.
12	110.6	11.9	558	10	AM036252 EST278331

13	109.8	11.8	775	11	BG645553	BG645553 EST507172
14	109.8	11.8	809	11	BG585146	BG585146 EST486909
15	109.2	11.8	810	11	BG646052	BG646052 EST507671
16	107.6	11.6	834	11	BG585934	BG585934 EST487699
17	107.4	11.6	583	10	A1812774	A1812774 18H7 pine
18	104.6	11.3	749	11	BG886881	BG886881 EST512732
19	103	11.1	728	11	BG597062	BG597062 EST495740
20	102.6	11.1	666	11	B1210187	B1210187 EST528227
21	101	10.9	608	10	AM735876	AM735876 EST336644
22	101	10.9	802	11	B1207010	B1207010 EST525050
23	100	10.8	768	11	BG643290	BG643290 EST511484
24	99.2	10.7	805	10	AT1725905	AT1725905 BNLGH1134
25	98.2	10.6	717	10	AM623899	AM623899 EST321844
26	97	10.5	450	11	B1204344	B1204344 EST522284
27	97	10.5	516	11	B1211043	B1211043 EST529083
28	97	10.5	546	11	B1204893	B1204893 EST522933
29	97	10.5	725	11	B1203937	B1203937 EST521977
30	97	10.5	727	11	B1204715	B1204715 EST522755
31	97	10.5	727	11	B1205090	B1205090 EST523130
32	96	10.4	487	11	BR096480	BR096480 EST560507
33	95	10.2	785	11	B1206688	B1206688 EST524728
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35	92.8	10.0	592	10	AM934320	AM934320 EST360163
36	92.4	10.0	663	11	B1270081	B1270081 NF004A12F
37	92.2	9.9	742	11	BG125807	BG125807 EST471453
38	91.2	9.8	565	11	B1140861	B1140861 IPL_40_A0
39	88.6	9.6	423	10	AM278395	AM278395 s43e12.y
40	87.8	9.5	625	13	A0842192	A0842192 T134491.S
41	86.8	9.4	486	10	BE499582	BE499582 WHE0962_G
42	86.6	9.3	569	11	B1076149	B1076149 IPL_26_BO
43	85.4	9.2	613	10	BE511087	BE511087 sq75b01.y
44	84.8	9.1	778	11	BG128733	BG128733 EST474379
45	84.2	9.1	587	13	B24616	B24616 F21A23TR IG

ALIGNMENTS

RESULT 1
BG129531
LOCUS BG129531 673 bp mRNA EST 31-JAN-2001
DEFINITION EST475177 tomato shoot/meristem Lycopersicon esculentum cDNA clone
CTOF24H8 5' sequence, mRNA sequence.
ACCESSION BG129531
VERSION BG129531.1 GI:12629719
KEYWORDS EST.
SOURCE
ORGANISM
tomato.
Lycopersicon
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 673)
REFERENCE
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Romning,C. and Tankley,S.
Generation of ESTs from tomato shoot/meristem tissue
Unpublished (2001)
COMMENT
Contact: CGCI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.
location/Qualifiers
1. 673
/organism="Lycopersicon esculentum"
/cultivar="FA496"
/db_xref="taxon:4081"
/clone="CTOF24H8"
/clone_lib="tomato shoot/meristem"
/rissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

DB	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	306	TAAGTCTTCATATTGCGATTCACCACTATATTCAGACGCTCAGAGGATTTGACT	365					
Oy	662	TTTGGAGTTTAAAGACCTTCTGAAGCTGCTGCTGTGCGACCTTTCTGTTTCGAGAAAT	721					
Db	366	TCTTGTGATTTTAAACCATCAGAGATTGGACGACGAGCTGCTATGTATGTCATGGGGGAA	425					
Oy	722	TGCGAGAGGTACACTTTTACACACTCTTCCTCTCCCTTTTCTTCACACTTCAAAAG	781					
Db	426	CCCAACAGCTTGACACTGGAA---AGCAATCTCTGTTCTGATTCACACAGTAGAATAGG	482					
Oy	782	AGAGAGTGAAGATATAGGCGAATATGAT	809					
Db	483	AGAGACTATTGTAAGTGTTCATAATGAT	510					
RESULT	3							
LOCUS	AI728767	512 bp	mRNA	EST	11-JUN-1999			
DEFINITION	BNIGH11561 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (A011892) cyclin D2.1 protein [Nicotiana tabacum], mRNA sequence.							
ACCESSION	AI728767							
VERSION	AI728767.1	GI:5047619						
KEYWORDS	EST.							
SOURCE	upland cotton.							
ORGANISM	Gossypium hirsutum							
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.							
AUTHORS	Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.							
TITLE	ESTs from developing cotton fiber							
JOURNAL	Unpublished (1999)							
COMMENT	Contact: Ben Burr Biology Department Brookhaven National Laboratory Upton, NY 11973, USA Tel.: 516-344-3396 Fax: 516-344-3407 Email: burr@bnl.gov Seq primer: 73 primer.							
FEATURES								
SOURCE	Location/Qualifiers							
	1. 512							
	/organism="Gossypium hirsutum"							
	/cultivar="Acala Maxxa"							
	/db_xref="taxon:3635"							
	/clone_lib="Six-day Cotton fiber"							
	/library_type="Immature fiber"							
	/dev_stage="Six days post anthesis"							
	/lab_host="XL1-Blue"							
	/note="Vector: pBluescript II KS+"							
BASE COUNT	146 a 86 c 113 g 167 t							
ORIGIN								
Query Match	18.3%;	Score 169.2;	DB 10;	Length 512;				
Best Local Similarity	74.8%;	Pred. No. 2.1e-33;						
Matches 226;	Conservative 0;	Mismatches 73;	Indels 3;	Gaps 1;				
Oy	125	AGAGTGAAGATTTTCATGAGATGCTGCGAAGAGAGACAGCATTTGCCAAGTGATG	184					
Db	214	AAAGTGATGATCGAATCAAAAGATGTTGAAAGAGGTGAGCATTTGGCCTGAAGATG	273					
Oy	185	ATTATCTACAGAGACTTGAAGTGAAGATTTGAAATGTTGGAAGACAGATGCC	244					
Db	274	ATTATCTACAGAGACTGAGAAAGTGGGATTTGACTTGAGTGT---ACGAAGAGGCTC	330					
Oy	245	TCAATTTGATTTGAAGGCTTGTGAAGTACACAGATTTGACCATTTGCTTTTGCTTAG	304					
Db	331	TTCATTTGATTTGAAGGCTTGTGCTTATTAAGTTTTGACCTTTGATCTTTGCTAT	390					
Oy	305	CAATGACACTTGGATGATCTTATCGCTTCATGATTTGGCTAGTGGCAAGGTTGCA	364					

Db	391	CCATTAACTACTTGATGGATCGGCTTCCTTTCAGTTTATGACTTACTAGAGTAACATGCA	450
Qy	365	TATTCGACGTGTGGCTGTGGCTGTGTTATATCATTTGGCAGCCAAATTTGAAGAATGAA	424
Db	451	CCGTCACAAATTCCTGTCTGTGCTGTATATCAATTTGCACCCAAATGAGAGACAAAG	510
Qy	425	TT 426	
Db	511	TT 512:	
RESULT	4		
LOCUS	B1306295/c	790 bp	mRNA
DEFINITION	NL_4_B12 Drought stress (leaf) Oryza sativa cDNA clone NL_4_B12 3'	EST	20-JUL-2001
ACCESSION	B1306295		
KEYWORDS	B1306295.1 GI:14981617		
SOURCE	EST.		
ORGANISM	Oryza sativa.		
REFERENCE	Oryza sativa.		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzaceae; Oryza.		
TITLE	1 (bases 1 to 790)		
JOURNAL	Reddy A.R., Kamakrishna, W., Chandrasekhar, A., Nagabushan, I., Ravindrababu, P. and Bennetzen, J.L.		
COMMENT	Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L. cv Nagina 22)		
FEATURES	Unpublished (2001)		
SOURCE	Contact: Reddy AR		
	Department of Plant Sciences, School of Life Sciences		
	University of Hyderabad		
	P.O. Central University, Hyderabad-500 046, A.P., India		
	Tel: 0091-40-3010265		
	Fax: 0091-40-3010145		
	Email: arjuls@uohyd.ernet.in		
	Insert Length: 790		
	Plate: 4		
	row: B		
	column: 12		
	Std Error: 0.00		
	Seq primer: GTAAACGACGCCGATGTCG.		
	Location/Qualifiers		
	1..790		
	/organism="Oryza sativa"		
	/cultivar="Nagina 22 (Indica sub sp)"		
	/db_xref="taxon:4530"		
	/clone="NL_4_B12"		
	/clone_lib="Drought stress (leaf)"		
	/tissue_type="entire leaf tissue"		
	/dev_stage="35 day-old seedlings"		
	/note="Organ: Leaf; Vector: T73Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"		
BASE COUNT	222 a	239 c	179 g 150 t
ORIGIN			
Query Match	17.6%	Score 163.4:	DB 11: Length 790:
Best Local Similarity	58.7%:	Pred. No. 7.3e-32:	
Matches	322:	Conservative	0: Mismatches 221: Indels 6: Gaps 2
Qy	130	GAGGAGATTATCATGACATGCTGGAGAGAGAGACAGCATTTGCCAAGTATGATTAC	189
Db	590	GATGAGTTCTGTGGCGTTGTTGGTGGAGAGATGATCATCAGCCTCAGCGGGGGTAT	531
Qy	190	ATCAAGAGACCTAGAAAGTGGAGATTTGGATTGGAATGTTGGAAGAGAGATGCCCTCAT	249
Db	530	CTGGAGAACCTGGAGCTCGGTGGATTGGA---GTGTTCTTGGAGGAAAGATGCAATTGAT	474
Qy	250	TGATATTGGAAAGCTTGTGAAAGTACACCAAGTTTGGACATTTGTTTGTCTTAGCAATG	309
Db	473	TGGATTTCGAAGCTGCATTCCTACACCACTTTGGACCACTCAGCCTTACCTCGCAGTG	414
Qy	310	AACACTTGGATGATTTCTTATCGGTTATGATTTGCCTAGTGCCAAAGCTTGATATTG	369

Db 413 AACTAACGTGATAGAGTTCCTCCTCCGTTTAATCTCCATGACGATCTTGATGCAA 354

QY 370 CAGTTGTTGGCTGTGGCTTGTATCATTTGCGAACCAATTTGAGAATCTGAGTTCCA 429

Db 353 CAGTTGCTCTCAGATTAGTTGTCTATCTCTTGTACGAATGAGAGACCGGTGCTCT 294

QY 430 AAGTTGATGATCTTCAGTTGGAGATCCTCAAGTTGTTGGAGCTTAATGAGTCAA 489

Db 293 CTTCCTCATGCTTCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 234

QY 490 AGAATGAGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 549

Db 233 AGAATGAGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 174

QY 550 TCATACATTAAGATTTCTCTGAGAAAGATGATTAATTTGATCAGAACCATTCACA 609

Db 173 TCTTTCATGCGCTACTTCTCGACCAAGTTCAATGAGGAGAGC---GCGGAGCTTCACAG 117

QY 610 TTGATATCTAGATCAATTAAGATGAGGACGACACCAACCAAGTATTTGACTTTTGGAG 669

Db 116 CTGGCATCTAGGCTGCTCTGATCTCACAGTGGCAGCTCTGAAGACTCTAGGTTCTTGTA 57

QY 670 TTAGACCT 678

Db 56 TTCAGACCT 48

RESULT 5

LOCUS A1728683 562 bp mRNA EST 11-JUN-1999

DEFINITION BN1GH11316 six-day cotton fiber Gossypium hirsutum cDNA 5' similar to (A011892) cyclin D2.1 protein [Nicotiana glauca], mRNA sequence.

ACCESSION A1728683

VERSION A1728683.1 GI:5047535

KEYWORDS EST.

SOURCE upland cotton.

ORGANISM Gossypium hirsutum

REFERENCE Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

AUTHORS 1 (bases 1 to 562)

TITLE Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.

JOURNAL ESTs from developing cotton fiber

COMMENT Unpublished (1999)

CONTACT: Ben Burr

Biology Department

Brookhaven National Laboratory

Upton, NY 11973, USA

Tel: 516-344-3396

Fax: 516-344-3407

Email: burr@bnl.bnl.gov

Seq primer: 73 Primer.

FEATURES

Location/Qualifiers

source

1..562

/organism="Gossypium hirsutum"

/cultivar="Acala Maxxa"

/db_xref="taxon:3635"

/clone_lib="Six-day Cotton fiber"

/tissue_type="Immature fiber"

/dev_stage="Six days post anthesis"

/lab_host="XL1-Blue"

/note="Vector: pBluescript II KS+"

BASE COUNT 156 a 101 c 117 g 186 t 2 others

ORIGIN

Query Match 16.5%; Score 153; DB 10; Length 562;

Best Local Similarity 69.8%; Pred. No. 3.4e-29;

Matches 220; Conservative 0; Mismatches 92; Indels 3; Gaps 1;

QY 114 TTCTCAATCGAGAGTGAAGATTATCATGAGATGGTGAAGAGAGAGAGCATTT 173

Db 244 TTTTGATTAACAAGATGATGATTAATTAAGCAATGTTGAAGAGATGAGCATTT 303

QY 174 GCCAAGTATGATTTACATACAGACTTGAAGTGAAGATTGGATTGAATTTGAAG 233

Db 304 GCCATAGATGATTAATTAATTAAGACTGAGAACTGGGAGATTGGAGTTGA---GCGCCAC 360

QY 234 AAGAGTGGCCCAATTTGATTTGGAAGCTTGAAGTACACACTTTGGACATTTGG 293

Db 361 GAGAGAGCTTGAATGATTTGAAGGCTTCANCTTAATTTCAATTTGGAGCTGTAG 420

QY 294 TTTTGCTTGAAGTAACTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 353

Db 421 TCTTTCATATCATTAATTAATTAAGCTGATTTGATTTGATTTGATTTGATTTGATTTG 480

QY 354 CAAAGTTGATTAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 413

Db 481 TAAACATGACTTCACAACTGTGGCCGTGATTTATTAATTAATTAATTAATTAATTA 540

QY 414 AGAAGTGAAGTTCC 428

Db 541 GGAACCAAGGTGCC 555

RESULT 6

LOCUS CDS00055 381 bp DNA GSS 28-JUN-1999

DEFINITION Arabidopsis thaliana genome survey sequence Sp6 end of BAC T8D11 of TAMU library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.

ACCESSION AL090574

VERSION AL090574.1 GI:5291714

KEYWORDS GSS.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

AUTHORS 1 (bases 1 to 381)

TITLE Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 381)

AUTHORS Unpublished

TITLE Genoscope.

JOURNAL Direct Submission

COMMENT Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage; BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

FEATURES

Location/Qualifiers

source

1..381

/organism="Arabidopsis thaliana"

/strain="Columbia"

/db_xref="taxon:3702"

/clone_lib="TAMU"

/clone="T8D11"

/note="end: Sp6"

BASE COUNT 140 a 42 c 69 g 130 t

ORIGIN

Query Match 16.1%; Score 149.2; DB 13; Length 381;

Best Local Similarity 92.4%; Pred. No. 3e-28;

Matches 157; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 758 CTTCTTTCACACTCTTCAAAAGAGAGAGTGAAGAGATGAGGGGAAATGATGAGAGTG 817

Db 5 CTTTGTGTTCTTTTATTTGACAGAGAGTGAAGAGATGAGGGGAAATGATGAGAGTG 64

QY 818 ATGGCTCAGACTTATTTGACAAACCAATGAGGCTTTTGAAGATGAGGCTTGTGTT 877

Db 65 ATGGCTCAGACTTATTTGACAAACCAATGAGGCTTTTGAAGATGAGGCTTGTGTT 124

QY 878 TTAGCTTAAGACCAATGATTTCTTCTTCTTATACATCTTTCTTAA 927

DB	125	TCAGCTTAAACAGCCATGATCTCTCTCTCTCTCTCTTAAACAGCATCTTCTTAA	174
RESULT	7		
LOCUS	BE442681		
DEFINITION	BE442681 621 bp mRNA EST 25-JUL-2000		
VERSION	WHE1101.A09.A17S	Wheat etiolated seedling root normalized cDNA	
KEYWORDS	library Triticum aestivum cDNA clone WHE1101.A09.A17, mRNA		
SOURCE	sequence.		
ORGANISM	BE442681 GI:9442114		
REFERENCE	EST.		
AUTHORS	bread wheat.		
	Triticum aestivum		
	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae		
	; Triticeae; Triticum.		
	1 (bases 1 to 621)		
	Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han		
	, P.S., Heia, C.C., Kang, Y., Iazo, G.R., Miller, R., Nguyen, H.T.,		
	Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.		
	The structure and function of the expressed portion of the wheat		
	genomes - Normalized root cDNA library		
	Unpublished (2000)		
JOURNAL	Contact: Olin Anderson		
COMMENT	US Department of Agriculture, Agriculture Research Service, Pacific		
	West Area, Western Regional Research Center		
	800 Buchanan Street, Albany, CA 94710, USA		
	Tel: 5105595773		
	Fax: 5105595818		
	Email: oanderson@w.usda.gov		
	Sequence have been trimmed to remove vector sequence and low		
	quality sequence with phred score less than 20		
	Seq primer: Stradgene SK primer.		
FEATURES	Location/Qualifiers		
source	1..621		
	/organism="Triticum aestivum"		
	/cultivar="Chinese Spring"		
	/db_xref="taxon:4565"		
	/clone="WHE1101.A09.A17"		
	/clone_lib="Wheat etiolated seedling root normalized cDNA		
	library"		
	/tissue_type="Root"		
	/dev_stage="five day old etiolated seedling"		
	/lab_host="E. coli DH10B"		
	/note="Vector: Lambda Uni-ZAP XR, excised phagemid		
	pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were		
	surface-sterilized, germinated and grown aseptically in		
	the dark at room temperature on filter paper with water,		
	nystatin and cefotaxime in covered crystallization		
	dishes. Roots were harvested. The tissue, total RNA, and		
	poly(A) RNA were prepared, a cDNA library was made in the		
	TJ Clones lab (Choi, Close, Fenton) at the University of		
	California, Riverside. The cDNA clones were in vivo		
	excised to give pBluescript phagemids before		
	normalization and normalization were done in HT Nguyen		
	lab by D. Zhang at Texas Tech University. Normalization		
	protocol used was that of Soares. Plasmid DNA		
	preparations and DNA sequencing were performed in the OD		
	Anderson lab (all other authors)."		
BASE COUNT	142 a 157 c 156 g 166 t		
ORIGIN			
Query Match	16.1%; Score 149.2; DB 10; Length 621;		
Best Local Similarity	60.6%; Pred. No. 3.4e-28;		
Matches 263; Conservative 0; Mismatches 168; Indels 3; Gaps 1;			
266	CCATGTCGTTTGGCTTACGATGACACACTGCTGCATGATCTCTTATCGGTTATGATTTG	345	
1	CCGTTACGCGCGCTCTGCTGTCACACACTGTTAGAGTGCTCTCCCTCATATCCCTT	60	

Query Match	13.3%	Score 123.6	DB 10	Length 813
Y	346	CCTAGTGGCAAAAGGTGGATATTGACAGTTGTTGGCTGGGCTGTGTTATTCATTGGCAGCC	405	
Db	61	CCTAAGGCAAAAGCTTGGGTGACACAGCTCTTGCGCAGTGCTGTCTGCTCCCTTC	120	
Y	406	AAATTTGAAGAACTGCAAGTTCCAAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTTT	465	
Db	121	AAGATTTGAGAGACCTATGTCGCCGTCCCGTCGACCTCGAGGTGTTGAGGCAAAATTC	180	
Y	466	GTGTTTGAGGCTAAATATGATCCAAAGAAATGAGAGCTTTTGGTGTGACAAATGAAATGG	525	
Db	181	GCGTTTCGAGGAGAACCATTAAGAAAGATGAGAGCTTTTGGTGTGACCACTTAAGATGG	240	
Y	526	AGATTGAGAGCAATTAACCTCCATGCTCAATACATTAATGATATTTTCTCGAAGAAATGAGTAAA	585	
Db	241	AGGATGCAAGCTGTATGCTGCTGCTCATTATTAATGACTCTTCGCAAAATTCATATA	299	
Y	586	TGTGATCAAGAACCATTCACACATTTGATATTCATATTAACAGATATGACCAACA	645	
Db	300	--TCATGACGCGCCCTCCATGCTGCGATTTCCGCCCTGACGACCTCATCTGAGCACA	357	
Y	646	ACCAAAAGTATTTGATTTTGGAGATTGAGACCTTCGAAAGCTGCTGCTGTGGCAGTT	705	
Db	358	GCTAAAGAGAGCTGATTTTGTGTGTTACAGACCTTAGAGATGCTGCAAGTGTCCAGCTT	417	
Y	706	TCTGTTTCTGAGCA	719	
Db	418	GCCGCATTGTTGGGGA	431	
RESULT	8			
LOCUS	BE642779			
DEFINITION	BE642779	813 bp	mRNA	EST
ACCESSION	BE642779			01-SEP-2000
VERSION	BE642779.1	GI:3960458		
KEYWORDS	EST.			
SOURCE	Ceratopteris richardii.			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
REFERENCE	1 (bases 1 to 813)			
AUTHORS	Chatterjee, A., San Miguel, P., Stout, S.C., Banks, J. and Roux, S.J.			
TITLE	Expressed sequence tags of cDNA clones from a C. richardii library			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Roux SJ			
	Section of Molecular Cell and Developmental Biology			
	University of Texas			
	Biology Building, Room 16, Austin, TX 78712, USA			
	Tel: 512 471 4238			
	Fax: 512 232 3402			
	Email: sroux@uts.cc.utexas.edu			
	Plate: Ctr12.6 row: P column: 20			
	Seq primer: SP6.			
FEATURES	Location/Qualifiers			
source	1..813			
	/organism="Ceratopteris richardii"			
	/cultivar="Brogn"			
	/db_xref="taxon:49495"			
	/clone="Ctr12.6_P20"			
	/clone_1lb="Ceratopteris Spore Library"			
	/tissue_type="Gametophyte"			
	/cell_type="Spore"			
	/dev_stage="20 hours after germination initiation"			
	/note="vector: pCMVSPORT6; EST sequence from cDNA library			
	cDNA library constructed from mRNA isolated from C.			
	richardii spores that had developed for 20 hours after			
	their germination had been initiated by white light."			
BASE COUNT	196 a 169 c 191 g 257 t			
ORIGIN				

							/lab_host="DH10B"
						:/note=vector: plulescript II SK+, Site_1: EcoRI; Site_2:	
						XhoI; The cdna library was constructed from mRNA isolated	
						from mature seed pods of greenhouse grown plants prior to	
						sensescence for the cultivar KP1. Complementary DNA was	
						synthesized from mRNA using a primer consisting of a	
						poly(ctf) sequence with a XhoI restriction site. EcoRI	
						adapters were ligated to the blunt-ended cDNA fragments	
						followed by XhoI digestion. The cDNA fragments were	
						directionally cloned into the EcoRI-XhoI restriction site	
						of the pbluescript vector. The ligated cDNA fragments	
						were transformed into DH10B host cells (GibcoBRL). This	
						library was constructed in the laboratory of Dr. Randy	
						Shoemaker."	
BASE COUNT	136 a	83 c	107 g	172 t	.		
ORIGIN							
Query Match	12.0%;	Score 111.6;	DB 11;	Length 498;			
Best Local Similarity	66.9%;	Pred. No. 1.9e-18;					
Matches 153;	Conservative	0;	Mismatches 69;	Indels 0;	Gaps 0;		
QY	228 TGGGAAGACGATGCCCTCAATTGGATTGTGAAGCGTTTGAAATCACACCAGATTGGACC	287					
Dd	14 TGTTAAGAAGAGCCTCTTCGATTGCATTTTGGAAAGCCTCATGCTACTTTGGACTTTGGACC	73					
XY	288 ATTGTGTTTTGCTTAGCAATGCAACTACTTCGGATTTCATTATGGGTTCCATGAAATTTGCC	347					

OY	348	TAGTGGCAAGAGTTGGATTATTTGCAGCTTGTGGCTGTGGCTTTATCATTTGGACGCCAA	407
Db	134	AAGAGGCAAAAGTTGGACTATGCAACCTCTTACCTGTACCATCTTTGTCATTGCTGCCAA	193
OY	408	AATTGAGAAACTGACAGTCTCCATCTTATATGACTTTACGT	449
Db	194	AATGGAGGAGATTAAAGTGCCCTCTTGATGAGATTACAGGT	235

RESULT 12

ACCESSION	AM036252
VERSION	AM036252.1
KEYWORDS	GI:5895006
SOURCE	EST.
ORGANISM	tomato. Lycopersicon esculentum
REFERENCE	Eukaryotes: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots; Asteridae: euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
AUTHORS	1 (bases 1 to 558) Alcala,J., Vrebalov,J., White,R., Mattern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craigmiles,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,C.B., Tanksley,S.D. and Giovannoni,J.
TITLE	Generation of ESTs from tomato seed tissue
JOURNAL	Unpublished (1999)
COMMENT	Contact: CUGI Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.

```

FEATURES
  source
    location/Qualifiers
      1..558
        /organism="Lycopersicon esculentum"
        /cultivar="TA96"
        /db_xref="taxon:4081"
        /clone="cLEE2D20"
        /clone_id="tomato seed, TAMU"

```

```

/lisse_type="seeds"
/dev_stage="quiescent seed"
/lab_host="XLI-Blue MR#"
/note=Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLE: - Tomato Seed EST library. Directionally cloned
cDNAs inserted into pBluescript SK(-) at 5' end with
EcoRI and 3' end with XhoI site."
BASE COUNT      149 a      111 g      201 t
ORIGIN

Query Match      11.9%; Score 110.6; DB 10; Length 558;
Best Local Similarity 57.8%; Pred. No. 3.5e-18;
Matches 197; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

OY 238 GATGCCCTCAATTGATTTGGAAAGCGCTGTGGAATGACACCAAGTTGGACATTTGGTTT 297
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 GATGTGTGTTGAATGATCTTCTTAAAGTGAAGCTCAATTTATGATTTCTCAGCATTTGCTCC 208

OY 298 TGCTTAGCAATGAACTACTGTGGATGGATTCTTAAGGTTTCATGATTTGGCTGTAGTGGCAA 357
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 ATTTTAGCCATTAAATTAATCTTTCAGAGTTTCTTTCTAGCCCTTCAATTCAGAAAGATAAG 268

OY 358 GGTGTGATATTGACAGTTGTGGCTGTGGCTGTTTATCATTTGGACGCCAAATTAAGAA 417
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 CCATGGATGACCAACTGTCTGTCTCATCTTCTTTCTTTAGCGGCTTAAGATTAAAGAA 328

OY 418 ACTGAAGTTCCAAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTTGCTGTTGAGGCT 477
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 ACTCAAGTTCCCTCTCTCTTCTGACTTCCAAAGTGAGAGATGCAAAATATGCTGTTTAGGCA 388

OY 478 AATATGATGCCAAAGATGAGCTTTTGGTGTGAACAATTAATTAATGAGATTGAGAGCA 537
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 AAGACTATTAACAAGATGAGAGCTCTGTGATCTCATCTGAATGAGAGATGATATCA 448

OY 538 ATAACCTCATGCTCATACATAGATTAATTTCCAGAGAAAGAT 578
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 GTACCCCACTTTCATTTCTTGATCATATTAATAAGAGGCT 489

RESULT 13
LOCUS      BG645553      775 bp      mRNA      EST      24-APR-2001
DEFINITION EST507172 KV3 Medicago truncatula cDNA clone pkV3-46023 5' end,
      mRNA sequence.
ACCESSION   BG645553
VERSION     BG645553.1 GI:13780665
KEYWORDS
SOURCE      EST.
ORGANISM    barrel medic.
            Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
            Medicago.
            1 (bases 1 to 775)
            Vandenbosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Bowman
            ,C.B., Craven,M.B., Cho,J. and Fraser,C.M.
            ESTs from roots of Medicago truncatula 72 h after Rhizobium
            inoculation, 2001
            Unpublished (2001)
            Contact: Vandenbosch K
            Department of Biology
            Texas A&M University
            College Station, TX 77843-3258, USA
            Tel: 409 845 7707
            Fax: 409 845 2891
            Email: kate@mail.bio.tamu.edu
            M333960e TIGR sequence name: MTECC60TR More information is
            available at: www.medicago.org
            Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
            Location/Qualifiers
            ..775
            /organism="Medicago truncatula"

```

Query Match	Best Local Similarity	Matches	Score	DB	Length
11.8%;	50.7%;	0;	109.8;	DB 11;	775;
Conservative	0;	Mismatches	302;	Indels	6;
					gaps
					2;
123	GGAGAGTGAGAGATTTATCATGTAGAGATGTTGGAGAGAGAGAGAGATTTGCCAAGTGA	182			
127	GGAGAGAGAGAGAGATTTATCATGTAGAGATGTTGGAGAGAGAGAGAGATTTGCCAAGTGA	186			
183	TGATTTACATCAAGAGATTTAGAGATGAGATTTGGATTTGAATGTTGGAGAGAGATGC	242			
187	CGAGTACGCTTCAGATTTCCAAATCTCGCTCTCGAATCA--GCACAGAGAGAGAGAGC	243			
243	CCTCAATTTGATTTTGAAGGCTTGTGAAGTACACAGTTTGAGACATTTGTTTGTGCTT	302			
244	CATTGCATGAGATTTCCAAAGTACATGATTAATGATTAATGATTAATGATTAATGATTAATG	303			
303	AGCATGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	362			
304	CTCGTTTACATTAATGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	363			
363	GATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	422			
364	GCACTGCACTTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	423			
423	AGTTCCAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	482			
424	GTTTCTTCTCTCTTCACTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	483			
483	AGTCCAAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	542			
484	GATTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	543			
543	TCCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	602			
544	CCCCTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	600			
603	CACACATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	662			
601	CCACTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	660			
663	TTTGGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	722			
661	TCTTACTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	720			
723	GCAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	747			
721	TCTTAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	745			

RESULT 14

LOCUS BG585146

DEFINITION EST486909 MHAM Medicago truncatula/Genom versifforme mixed EST library cDNA clone pMHAM-22A23 5' end, mRNA sequence.

BASE COUNT 183 a 185 c 167 g 240 t

ORIGIN

/cultivar="genotype A17"

/db_xref="taxon:3880"

/clone="pkv3-46J23"

/clone_id="RV3"

/tissue_type="Seedling roots"

/dev_stage="3 days post-inoculation with Sinorhizobium meliloti"

/lab_host="E. coli strain XLOLR"

/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the unizap XR vector from StrataGene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in XLOLR cells."

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BC585146	1	GI:13600210							
BC585146.1									
EST									
Medicago truncatula/Glomus versiforme mixed EST library.									
Medicago truncatula/Glomus versiforme mixed EST library									
Eukaryota: mixed EST libraries.									
1 (bases 1 to 809)									
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Uterback,T., Cho,J.									
and Fraser,C.M.									
ESTs from roots of Medicago truncatula after colonization with									
Glomus versiforme, 2001									
Unpublished (2001)									
Contact: Harrison M.J.									
Plant Biology Division									
The Samuel Roberts Noble Foundation									
2510 Sam Noble Parkway, Ardmore, OK 73401									
Tel: 580-223-5810									
Fax: 580-221-7380									
Email: mharrison@noble.org									
Noble EST name: N380619e TIGR sequence name: MTDCAL2TK More									
Information is available at: http://www.medicago.org									
Seq primer: SKmod (CTA GAA CTA gta gat CC).									
Location/Qualifiers									
1..809									
/organism="Medicago truncatula/Glomus versiforme mixed EST									
library"									
/cultivar="Medicago truncatula genotype A17"									
/db_xref="taxon:119092"									
/clone="pMHAM-22A23"									
/clone.lib="MHAM"									
/tissue_type="Roots colonized with Glomus versiforme"									
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days									
post-inoculation with Glomus versiforme. The library was									
made from a mixture of RNA from each of these stages."									
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directionally ligated into the UniZap XR vector from									
stratagene and packaged using Gigapack III Gold packaging									
extracts. Plasmids containing cDNA inserts were excised									
from the recombinant lambda-Zap phage using Ex-assist									
helper phage and propagated in XLOLR cells."									
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213 CGACATGACGTCGAAGATTCATGCTCGCTCTCGAATCCA--GCACCAAGAGAAGAC	269								
243 CCTCATTTGGATTTGGAAGGCTTGTGAAGTACACCAAGTTTGACCAATTTGTTTGTCT	302								
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		Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;		
		Medicago.		
	REFERENCE	1 (bases 1 to 810)		
	AUTHORS	Vandenbosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Bowman		
		,C.L., Craven,M.B., Cho,J., and Fraser,C.M.		
	TITLE	ESTs from roots of Medicago truncatula 72 h after Rhizobium		
	JOURNAL	inoculation, 2001		
	COMMENT	Unpublished (2001)		
		Contact: Vandenbosch K		
		Department of Biology		
		Texas A&M University		
		College Station, TX 77843-3258, USA		
		Tel: 409 845 7707		
		Fax: 409 845 2891		
		Email: kate@mail.bio.tamu.edu		
		M394459e TIGR sequence name: MTECU46TK More information is		
		available at: www.medicago.org		
		Seq primer: SKmod (CTA GAA CTA gtc gat CC).		
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		was directionally ligated into the UniZap XR vector from		
		stragene and packaged using Gigapack III Gold packaging		
		extracts. Plasmids containing cDNA inserts were excised		
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		helper phage and propagated in XL0LR cells."		
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Matches 308; Conservative 0; Mismatches 288; Indels 6; Gaps 2;

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OY 183 TGATTACATCAGAGACTTAGAAGTGGAGATTTGATTTGAATGTTGAAGAAGAGATGC 242
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About: Results were produced by the GenCure software, version 4.5.
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 1 (bases 1 to 1179)
 de Veylder, L., De Almeida Engler, J., Bursens, S., Manevski, A.,
 Lescure, B., Van Montagu, M., Engler, G. and Inze, D.
 A new D-type cyclin of Arabidopsis thaliana expressed during
 lateral root primordia formation
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1179)
 AUTHORS de Veylder, L.
 TITLE Direct Submission
 JOURNAL Submitted (16-DEC-1998) De Veylder L., Department of Genetics, VIB,
 Laboratorium voor Genetica, K.L. Ledeganckstraat 35, Gent B-9000,
 BELGIUM

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1 (sites)
Kaneko,Y., Kotani,H., Nakamura,Y., Sato,S., Asamizu,E., Miyajima,N.
and Tabata,S.
REFERENCE
AUTHORS
TITLE
STRUCTURAL ANALYSIS OF ARABIDOPSIS THALIANA CHROMOSOME 5. V.
SEQUENCE FEATURES OF THE REGIONS OF 1,381,565 BP COVERED BY TWENTY
ONE PHYSICALLY ASSIGNED P1 AND TAC CLONES
JOURNAL DNA Res. 5 (2), 131-145 (1998)
MEDLINE 98344145
REFERENCE 2 (bases 1 to 88356)
AUTHORS Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (02-MAR-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research, 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see

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FEATURES
source
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MNA5
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Graal
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.cornell.gov/Graal-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://greml.inl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MON23 and the 3' clone is K1904.
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AUTHORS        Bevan, M., Bancroft, I., Mewes, H.W., Rudd, S., Lemcke, K. and
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JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 113053)
AUTHORS        EU Arabidopsis sequencing project.
TITLE          Submitted (28-Apr-2000) MIPS, at the Max-Planck-Institut fuer
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                lemcke@mips.biochem.mpg.de, mayere@mips.biochem.mpg.de, Project
                Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
                Laboratory, John Innes Centre, Colney Lane, NR4 7JY Norwich, UK,
                E-mail: michael.bevan@bsrc.ac.uk
COMMENT        Information on performance of analysis and a more detailed
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ACCESSION A85057
VERSION A85057.1 GI:6733798
KEYWORDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.

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REFERENCE 1 (bases 1 to 1284)
AUTHORS Murray,J.A.
TITLE PLANTS WITH MODIFIED GROWTH
JOURNAL Patent: WO 9842851-A 1 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1650)
Soul,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif
Plant Cell 7 (1), 85-103 (1995)
JOURNAL MEDLINE
REFERENCE 95210930
AUTHORS Murray,J.A.H.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REMARK 3 (bases 1 to 1650)
AUTHORS Murray,J.A.H.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-1996) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REMARK 4 (bases 1 to 1650)
REFERENCE Murray,J.A.H.
AUTHORS

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TITLE Direct Submission
JOURNAL Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
COMMENT On Mar 28, 1998 this sequence version replaced gi:1402895.
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ACCESSION A85077
VERSION A85077.1 GI:6733818
KEYWORDS
SOURCE Zea mays.

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ORGANISM Zea mays
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Murray, J. A.
TITLE PLANTS WITH MODIFIED GROWTH
JOURNAL Patent: WO 9842851-A 21 01-OCT-1998:
MORRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
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ACCESSION AC006592 AE012093
VERSION AC006592.5 GI:6598614
KEYWORDS HTG.

SOURCE
ORGANISM thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 102051)
Lin,X., Reul,S., Rounsley,S.D., Shea,T.P., Bentto,M.-I., Town,C.D.
Fuji,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,
Feildbyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Renning,C.M.,
Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., Vankken,S.E., Umayam,L.
Tallon,L.J., Gill,J.E., Adams,M.D., Carreira,A.J., Creasy,T.H.,
Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
Niernm,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
Venter,J.C.

TITLE
Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana
JOURNAL Nature 402 (6763), 761-768 (1999)
MEDLINE 20083487
PUBMED 10617197
REFERENCE 2 (bases 1 to 102051)
AUTHORS Lin,X.
DIRECT Submission

**JOURNAL
COMMENT**

Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced g1:4544435.
The sequence and annotation of chromosome 2 were merged from the individual clones on this chromosome after removing overlaps. For detailed information, please see the tigr web site (<http://www.tigr.org/db/at/cat.html>).

Genes were identified by a combination of three methods: Gene prediction programs including GNAAL (<http://arthur.epm.ornl.gov/pub/xyz/gnaal>), GeneFinder (Phil Green, University of Washington), GENSCAN (Chris Burge, <http://genome.csf.stanford.edu/GENSCAN.html>), and NetPlantGene (<http://www.cbs.dtu.dk/services/NetPlantGene/>), searches of the complete sequence against a peptide database and plant EST databases at TRGR, and manual curation based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNASCAN-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNASCAN-SE/>). Simple repeats were identified by RepeatMasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/Masnu/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T3J16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jining Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

Address all correspondence to: at@tigr.org.

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CDS

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40 nSerGIu...SerGIuIleIleMetGluMetValGluIleGluLysG 56
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73 AspleuAsnValaGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCy 89
68261 GATTTGCTGTT...CGAACCAAGCTTTCATTTGATTTCTAAAGCTATG 68215
89 sGIuVal..... 91
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VERSION X83369.1 GI:2995129
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1951)
Sonl,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif
Plant Cell 7 (1), 85-103 (1995)
JOURNAL
MEDLINE 95210930
REFERENCE
2 (bases 1 to 1951)
Murray,J.A.H.
Direct Submission
Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
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3 (bases 1 to 1951)
revised by [3]
AUTHORS
Murray,J.A.H.
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JOURNAL
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ACCESSION A85060
VERSION A85060.1 GI:6733801
KEYWORDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Heliantheae; Helianthus.
1 (bases 1 to 1788)
REFERENCE
Murray J.A.
PLANTS WITH MODIFIED GROWTH
Patent: WO 9842851-A 4 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
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236 CGACGCCGCCGAGTGTCTCC.....TATGATTTCGAATATTCCGCGC 276
42 LuSerGluGluIleIleMetGluMetValGluIubsgluIubsgluIleu 58
277 ACTTGTATGATGATCGCGAGGTTTATACAGACGAGAGAAAGTTCCGT 326
59 ProSerAspAspTyrIleLeuYsArgLeuArgSerGlyAspLeuAspLeu 75
327 CCAGGATTCATTCAGTCGAGCGCATTTCAATCCGAGTTCTCGATGCTTC 376
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574 TTCCTTCTATTCTTATGATCTCAGGTTGACAGTGCAGAAATATATTTC 623
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DEFINITION Antlirrhinum majus mRNA for cyclin D1 (cyclD1 gene).

ACCESSION AJ250396

VERSION AJ250396.1 GI:6448479

KEYWORDS cyclD1 gene; cyclin D1.

SOURCE snapdragon.

ORGANISM Antlirrhinum majus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Lamiales; Veronicaceae; Antlirrhinum.

REFERENCE 1 (bases 1 to 1162)

Gaudin, V., Lunness, P., Robert, P., Towers, M., Riou-Khamlich, C.,

Murray, J., Coen, E. and Doonan, J.H. The expression of D-cyclin genes define distinct developmental

zones in Antlirrhinum apical meristems and is locally regulated by

the cycloidea gene

unpublished

2 (bases 1 to 1162)

Doonan, J.H.

Direct Submission

Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Innes

Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM

location/Qualifiers

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ACCESSION   AJ250397
VERSION     AJ250397.1  GI:6448481
KEYWORDS
SOURCE      snapdragon.

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REFERENCE
AUTHORS
TITLE

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I; Lamiales: Veroniceae: Antirrhinum.
1 (phases 1 to 1140)

Gaudin, Y., Lunness, P., Fobert, P., Towners, M., Rlou-Khamilich, C., Murray, J., Coen, E. and Doonan, J.H.
The expression of D-cyclin genes define distinct developmental

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1140)
AUTHORS Doonan, J.H.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Innes
Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM

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ID AAC39981 standard; DNA; 1290 BP.
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XX AAC39981;
AC 17-OCT-2000 (first entry)
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XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
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XX 06-SEP-2000.
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ID AAV33884 standard; cDNA to mRNA; 1284 BP.
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AC AAV33884;

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XX 25-JAN-1999 (first entry)
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KW CDC; Rd; retinoblastoma; germination; flowering; seed; fruit;
KW root development; ds.
XX Nicotiana tabacum.
OS
PN MO9842851-A1.
XX
PD 01-OCT-1998.
XX
PF 24-MAR-1998; 98MO-EP01701.
XX
PR 26-MAR-1997; 97EP-0302096.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Murray JAH;
XX
PI WPI; 1998-532012/45.
XX
DR
XX
XX Regulating growth and structure of plants by modulating protein that
PT controls cell division - specifically a D-type cyclin, and related
PT chimeric genes and transformed cells and plants, used to alter
PT growth rate, flowering, seed production etc.
XX
PS Claim 14; p52-53; 75pp; English.
XX
CC This sequence represents the CYCD2.1 cDNA from Nicotiana tabacum which
CC encodes a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.
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DT  25-JAN-1999 (first entry)
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KW  CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
KW  root development; ds.
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OS  Zea mays.
XX
PN  W09842851-A1.
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PD  01-OCT-1998.
XX
PF  24-MAR-1998; 98MO-EP01701.
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PR  26-MAR-1997; 97EP-0302096.
XX
PA  (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI  Murray JAH;
XX
DR  WPI: 1998-532012/45.
XX
PT  Regulating growth and structure of plants by modulating protein that
PT  controls cell division - specifically a D-type cyclin, and related
PT  chimeric genes and transformed cells and plants, used to alter
PT  growth rate, flowering, seed production etc.
XX
PS  Claim 14; p64-65; 75pp; English.
XX
CC  This sequence represents the CYCD1:1 cDNA from Zea mays which encodes
CC  a D-type cyclin. The sequence can be used to alter the growth
CC  characteristics or architecture of plants by altering the (functional)
CC  level in the plant cells of a cell-division controlling protein that can
CC  bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC  Modulation of the cyclin gene is used to increase or decrease the growth
CC  rate, provide faster germination, reduce time to flowering, increase the
CC  number of flowers, seeds or fruits per plant, increase root development,
CC  reduce height and to delay flowering in a range of plants, e.g. legumes,
CC  grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC  carnation, chrysanthemum, rose, tulip, etc.
XX
SQ  Sequence 1846 BP; 448 A; 425 C; 514 G; 458 T; 1 other;
XX
XX
alignment_scores:
Quality: 621.50 Length: 356
Ratio: 2.762 Gaps: 10
Percent Similarity: 63.202 Percent Identity: 39.888
XX
alignment_block:
US-09-530-209A-2 x AAV33889
XX
Align seq 1/1 to: AAV33889 from: 1 to: 1846
XX
10 LeuendCysThrGluSerAsn.....ValAspAspGluG1 21
   |||||.....||| :||| |||||.....|||
349 CTGCTGTGCGCGGAGACAAACGCTGATTTCTGCGCTGAGCAGCATGG 398
   |||||.....||| :||| |||||.....|||
21 ymet..... 22
   |||||.....||| :||| |||||.....|||
399 GGAAGAGTCTCTGTGGCGCGCGCTACGCCCACTGACACCGTGC 448
   |||||.....||| :||| |||||.....|||
23 .....lleValAspGluThr 27
   |||||.....||| :||| |||||.....|||
449 CCGCCGCCCGCCGACCGGGGCTCGCGTGCATGGGATTTTGCAGGATTC 498
   |||||.....||| :||| |||||.....|||
28 ProileGluIleSerIleProGlnMetGlyPheSerGlnSerGluSerG1 44
   |||||.....||| :||| |||||.....|||
499 CCCTTG.....CTCTCGGA 512
   |||||.....||| :||| |||||.....|||

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seq_name: /SIDS2/gcdata/geneseq/geneseqn/MA2000.DAT:AAZ94581
seq_documentation_block:
ID      AAZ94581 standard: DNA; 1861 BP.
XX
AC      AAZ94581;
DT      18-JUL-2000 (first entry)
XX
XX      Maize cyclin D ZmCycD gene.
DE
XX      Maize: cyclin D; ZmCycD gene; CycD; cell division; cell cycle;
XX      transgenic plant; ss.
XX
XX      Zea mays.
OS
FH      Key      Location/Qualifiers
FH      F75..1351
FH      CDS      /tag= a
FT
FN      WO200017364-A2.
XX
XX      30-MAR-2000.
PD
PF      21-SEP-1999; 99WO-US21946.
XX
PR      23-SEP-1998; 98US-0101551.
XX
XX      (P10N-) PIONEER HI-BRED INT INC.
PA
PI      Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;
PI      Hoerster GJ;
DR      WPI: 2000-283589/24.
DR      P-PSDB: AAY79321.
XX
XX      Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
XX      related proteins and antisense RNA useful for control of cell cycle
XX      regulation
XX
XX      Claim 1; Page 115-117; 134pp: English.
XX
XX      The present sequence is that of an isoform of the maize ZmCycD
XX      gene that encodes cyclin D (CycD, see AAY79321), a protein necessary
XX      for progression from G1 into S phase. The encoded protein binds to
XX      CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma
XX      associated protein, releasing the E2F transcription factor which
XX      activates DNA synthesis. The invention provides maize CycD
XX      polynucleotides (see AAZ94581-84) and polypeptides (see AAY79321-24)
XX      that are involved in cell cycle regulation. Also provided are
XX      recombinant expression cassettes (including ZmCycD in sense or
XX      antisense orientation), host cells, transgenic plants (especially
XX      corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or
XX      oilseed brassica) and antibody compositions. A claimed method of
XX      modulating the level of CycD protein in a cell comprises
XX      transforming the cell with a recombinant expression cassette
XX      comprising a CycD polynucleotide linked to a promoter, and
XX      growing the cell for a time sufficient to induce expression of the
XX      polynucleotide sufficient to modulate (increase or decrease) the
XX      CycD protein in the cell. The CycD protein is present in an amount
XX      sufficient to alter cell division, increase the number of cells
XX      dividing, improve transformation frequencies, alter cell growth,
XX      increase the growth rate, increase crop yield, alter plant
XX      height or size, enhance or inhibit organ (seed, root, shoot, ear,
XX      tassel, stalk, pollen, stamen) growth, produce organ ablation,
XX      produce parthenocarpic fruits, produce male sterile plants,
XX      enhance embryogenic response, increase callus induction, provide
XX      positive selection, increase plant regeneration, alter the time
XX      that cells are arrested in G1 or G0 phase or in a particular cell
XX      cycle, improve response to environmental stress including
XX      dehydration, heat or cold, increase the number of pods per plant,
XX      increase the number of seeds per pod or ear, alter the lag time in
XX      seed development, provide hormone-independent cell growth, or

```


CC increase the growth rate of cells in bioreactors. The level of
CC CycD protein in the cells is transiently modulated by introducing
CC CycD RNA or CycD polypeptides. CycD polynucleotides can be used
CC to identify CycD interacting proteins. All claimed.

XX Sequence 1861 BP; 462 A; 413 C; 512 G; 474 T; 0 other;

alignment_scores:

Quality:	621.50	Length:	356
Ratio:	2.762	Gaps:	10
Percent Similarity:	63.202	Percent Identity:	39.888

alignment_block:

us-09-530-209a-2 x AA294581 ..

Align seg 1/1 to: AA294581 from: 1 to: 1861

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308 CTGCTGTGGCGGAGAGCAACGCTGCTATTCTGGCTGAGCAGCATGG 357
21 yMet..... 22
358 GGAGGAGTCTCTCTGGGCGCGCGCTACGCCGACGTGACACCGTCG 407
23 .....IleValAspGluThr 27
408 CCGCCGCCGCCGCCACCGGGGTGCGCTCGATGGATTTTGACGGAGTTC 457
28 ProIleGluLeuSerIleProGlnMetGlyPheSerGlnSerGluSerG1 44
|||||.....|
458 CCCTTG.....CTCTCGGA 471
44 uGluIleIleMetGluMetValGluGluGluGlnHisLeuProSerA 61
|||||.....|
472 TGACTGGGTGGCAGCGCTCTGGAGAGAGAGGTGACACATGCCCCGG 521
61 spAspIlyrIleLysArgLeu.....ArgSerGlyAspLeuAsn 75
|||||.....|
522 AGGGGTACCTCCAGAACCTGCACGCGCATGGGCGCTGAGTTGGCC 571
76 ValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysGluValH1 92
|||||.....|
572 GCCGTGAGGAGAGACGCCATGATGGATTGGAGGTCAATTGACCTTA 621
92 sGlnPheGlyProLeuCySpheCysLeuAlaMetAsnTyIleuAspArg 109
|||||.....|
622 CAATTTCGACCGCTTGACTGCCGTTTGTCTGTGAACTACCTCGATGAT 671
109 heLeuSerValHisAspLeuProSerGlySgIyTrpIleLeuGlnLeu 125
|||||.....|
672 TCCTCTCCAGTATGATGCTCCGTAAGGAGAGGTTGATGAGTACACATC 721
126 LeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluGluThrGluVa 142
|||||.....|
722 TTGGCACTGCTGCTTGTCTTGGCTTGCAGAAATCGAAGAGACTTTTGT 771
142 lProMetLeuIleAspLeuGlnValGlyAspProGlnPheValPheGluA 159
|||||.....|
772 GCCACTCCCTCGATTTGCGAGTAGCGGAGGCAAACTTTGTTTATAGG 821
159 lAlysSerValGlnArgMetGluLeuValLeuAsnLysLeuLysTrp 175
|||||.....|
822 GAAGGACCAATAAAAGATGAGCTTCTGTGCTAACACACCTTAAAGTGC 871
176 ArgLeuArgAlaIleThrProCysSerTrpIleArgTrpPheLeuArgL 192
|||||.....|
872 AGCATGATGCTGTACTGCTGTCTCAATTGTTGAATACATTCTTCATAA 921
192 smetSerLysCysAspGlnIuProSerAsnThrLeuIleSerArgSerL 209
|||||.....|
922 ATTAGAGTGAT...CATGTGCACCCCTCTTGTGACACGCTCTGCTCTT 968

```

```

209 eugHValIleAlaSerThrThrylSgIyLleAspPheLeuGluPheArg 225
|||||.....|
969 CGGACCTGTGCTTGAGCACCGCTAAAGTGCTGTGATTCGTTTTCAGA 1018
226 ProSerGluAlaAlaAlaValAlaLeuSerValSerGlyGluLeuG1 242
|||||.....|
1019 CCTCCGAGATTCCTGCCAGTGTTCACCTTGCTCTGATTCGCGAATCAG 1068
242 nArgValHisPheAspAsnSerSerPheSerProLeuPheSerLeuLeu 259
|||||.....|
1069 GAGTTCGTATATTGAGAGAGCTGCTACTAGTCCAAATAT.....TTGG 1112
259 lnySGluArgValLysIleGlyLleMetIleGlu..... 271
1113 ACAAGAGAGGTTTAAAGATCCATGAATGATTCAAGAGACATTAAT 1162
272 .....SerAspGlySerAspLeuCySer..... 279
1163 GCGGAGACATTTGCTAAAGTGTGCTGATCATCAATCTCTGTGGCC 1212
280 .GlnThrProAsnGlyValLeuGluValSerAlaCys..... 291
|||||.....|
1213 ACAAGCCCAATAGGTCTCTGACGCTGCACGCTGTCTGATCAACAAA 1262
292 .....CysPheSerPheLysThr 297
1263 GCGATGACGCTACTGTGCGGTCTCTGCTGATGATTTAC..... 1300
298 HisAspSerSerSerSer 303
|||||.....|
1301 CATAGTCTTCCACACAGC 1318

seq_name: /SIDs2/gcdata/geneseq/geneseqn/AA2000.DAT-AA294582
seq_documentation_block:
ID AA294582 strand: DNA; 1077 BP.
XX
AC AA294582:
XX
DT 18-JUL-2000 (first entry)
XX
DE Maize cyclin D ZmCycD gene.
XX
KW Maize; cyclin D; ZmCycD gene; CycD; cell division; cell cycle;
XX transgenic plant; ss.
XX
OS Zea mays.
XX
PN WO200017364-A2.
XX
PD 30-MAR-2000.
XX
PF 21-SEP-1999; 99WO-US21946.
XX
PR 23-SEP-1998; 98US-0101551.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McEliver JA;
XX Hoerster GJ;
XX WPI: 2000-283589/24.
XX DR P-PSDB; AAT79322.
XX
PT Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
XX related proteins and antisense RNA useful for control of cell cycle
XX regulation
XX
PS Claim 1, Page 120-121; 134pp; English.
XX
CC The present sequence is that of an isoform of the maize ZmCycD
XX gene that encodes cyclin D (CycD, see AAT79322), a protein necessary

```


KW Maize: cyclin D; ZmCYCD gene; CycD; cell division; cell cycle;
 KW transgenic plant; ss.
 XX
 OS Zea mays.
 XX
 PN WO200017364-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 21-SEP-1999; 99WO-US21946.
 XX
 PR 23-SEP-1998; 98US-0101551.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;
 PI Hoerster GJ;
 DR WPI: 2000-283589/24.
 DR P-PSDB: AA79323.
 XX
 PT Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
 PT related proteins and antisense RNA useful for control of cell cycle
 PT regulation -
 XX
 PS Claim 1: Page 122-124; 134pp; English.

The present sequence is that of an isoform of the maize ZmCYCD gene that encodes cyclin D (CycD, see AA79323), a protein necessary for progression from G1 into S phase. The encoded protein binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AA794581-84) and polypeptides (see AA79321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCYCD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression of the polynucleotide sufficient to modulate (increase or decrease) the CycD protein in the cell. The CycD protein is present in an amount sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, tassels, stalk, pollen, stamen) growth, produce organ ablation, produce parthenocarpic fruits, produce male sterile plants, enhance embryogenic response, increase callus induction, provide positive selection, increase plant regeneration, alter the time that cells are arrested in G1 or G0 phase or in a particular cell cycle, improve response to environmental stress including dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in seed development, provide hormone-independent cell growth, or increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. CycD polynucleotides can be used to identify CycD interacting proteins. All claimed.

Sequence 1173 BP; 200 A; 366 C; 416 G; 191 T; 0 other:

alignment_scores:
 Quality: 554.50 Length: 345
 Ratio: 2.616 Gaps: 9
 Percent Similarity: 61.449 Percent Identity: 39.130

alignment_block:
 US-09-530-209A-2 x AA794583 ..

Align seg 1/1 to: AA794583 from: 1 to: 1173

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 37 CTCTCTGCGCGGAGAGACACAGCAGCTCTGTGTACGACAG..... 81
 22 ttleValAspGluThrProIleGluIleSerIleProGluMetGlyPheS 39
GAGGAGAGAGAGCTGGAGCGCGTGGAGGAGAGAGAGCGCGT 124
 39 erGluSer.....GluSer 43
 |||||.....
 125 CGCGCGGCTACGGGGAGACACTTCGCGCGGAGCTGTTCGCCCGCAGTCG 174
 44 GluGluIleIleMetGluMetValGluLysGluLysGluHisLeuProSe 60
 |||||.....
 175 GAGGAATGCGTGGCGCGCTGTGTGAGCGGAGACGACACATGCGCGG 224
 60 rAspAspTyrIleLysArgLeuArgSerGlyAspLeuAspLeuAsnValG 77

 225 GCGGTGCTACGGCGAGACAGCTGCGCGCGCGCGCTGTCTCTGCTC. 273
 77 LyArgArgAspAlaLeuAsnThrIleTyrLysAlaCysGluValHisGln 93
 274 ..CGCGGAGAGCGCGTGCACCTGATTTGGAAAGCTTACACCGCACACAG 321
 94 PheGlyProLeuCysPheCysLeuAlaMetAsnTyrLeuAspArgPhe 110
 |||||.....
 322 TTCCGCGCTCTACCTGCTTACTTGTGGCACTGATCCTGATCGCTTCT 371
 110 uSerValHisAspLeuProSerGlyLysGlyTyrIleLeuGluLeuAla 127
 |||||.....
 372 CTCTGCTGTGAGGTGCGGAGCGAGCTGATGCGAGCTCTCG 421
 127 IValAlaCysLeuSerLeuAlaAlaLysIleGluGluThrGluValPro 143
 |||||.....
 422 CGGAGCGCTGCTTCTCTGCGCGGCAAGATGAGAGAAACCGCGTCCG 471
 144 MetLeuIleAspLeuGluValGlyAspProGluPheValPheGluAla 160
 472 CAGTCCCGGACCTTACAGTGTGAGACCGCGGTACGTTCCGAGGCGAA 521
 160 sSerValGluArgMetGluLeuValLeuAsnLysLeuIleTyrPheGlu 177
 |||||.....
 522 GAGGTCCAGAGAGAGAGCTCTGTGTTTACACACCTTCAACAGGAGGA 571
 177 euArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgLysMet 193
 |||||.....
 572 TGCAATGCCGTGACCGCGTTCCTACGTGATTTACTTCTGACAAAGCTC 621
 194 SerLys..CysAspGluProSerAsnThrLeuIleSerArgSerLe 209
 622 AGCAACGCGCGACACAGCGCGCGGAGAGCTGCTGCTTGCATCTCCG 671
 209 uGluValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArgP 226

 672 GGAGCTTATCTTCTGCTGCGCGGAGAGACCGCTGCTGCGTTTCAGCC 721
 226 rSerGluAlaAlaAlaValAlaLeuSerValSerGlyGluLeuGln 242
 |||||.....
 722 CTGCGAATGCGCGCGCGGTGACCGCGGTGACCGCGGAGAGCTGAGC 771
 243 Arg.....ValHisPheAspAsnSerSe 250

 772 GACGCGAGCGCGCTGAGACACCGCTGCTGCTGCTGCTGCTGCTGCTG 813
 250 rPheSerProLeuPheSerLeuLeuGluLysGluArgValLysIleG 267
 |||||.....
 814AAGGAGCGGCTGTTGCGGTCC 835
 267 IyGluMetIleGluSerAspLysSerAspLeuCys..... 278
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836 AGGAGCGATCGGGTCCATGGCGTCTGGCGGCATTGACGGCGACGCT 885
278 ..... 278
886 ACCGTGCCACCGAAATCTGGAGACGACGAGCTCCCGCTGCCGTGCC 935
279 .....SerGlnThrProAsnGlyValLeuGluValSerAlaCysC 292
936 CGTGCCTGCGCCGACAGACCCCTGTGGGGGTGTGGAC...GCCGCGCCT 982
292 yspHeserPheLysThrHisAspSerSerSer 303
983 GCCTCAGCTACAGAGAGGACGACGACTCG 1017
seq_name: /SID52/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ19961
seq_documentation_block:
ID AAZ19961 standard; cDNA; 1932 BP.
XX
AC AAZ19961;
XX
DT 21-DEC-1999 (first entry)
XX
DE Corn cyclin delta-2 cDNA.
XX
KM Cyclin delta-2; corn; maize; cell cycle; cell division;
XX transgenic plant; herbicide; plant breeding; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 275..1441
FT /tag= a
XX
PN MO9948486-A2.
XX
PD 30-SEP-1999.
XX
PF 19-MAR-1999; 99MO-US06047.
XX
PR 23-MAR-1998; 98US-0078948.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
PI Cahoon RE, Klein TW, Odell JT, Orozco EM;
XX
DR MPI; 1999-591036/50.
XX P-PSDB; AAY31897.
XX
PT New isolated plant cyclin genes, used to develop products for use as
XX herbicides and for developing plant breeding programs -
XX
PS Claim 12; Page 56; 68pp; English.
XX
CC This nucleotide sequence represents a portion of the cDNA insert
CC in clone cels5.pk0049.h5 encoding a portion (see AAY31897) of a corn
CC cyclin delta-2 polypeptide. The clone was isolated from a corn
CC embryo (20 days after pollination) cDNA library. The invention
CC relates to isolated nucleic acid fragments (see AAZ19953-66) encoding
CC cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3
CC polypeptides (see AAY31889-902). It also relates to the construction
CC of chimeric genes encoding all or a portion of a cyclin, in sense
CC or antisense orientation, where expression of the chimeric gene
CC results in altered levels of the cyclin protein in a transformed
CC host cell. This would have the effect of altering the regulation
CC of cell division in those cells. The nucleic acid fragments may be
CC used to express cyclins in plant cells to enhance cell tissue
CC culture growth. The availability of nucleic acid sequences encoding
CC all or a portion of cyclins should facilitate studies of cell cycle
CC in plants, provide genetic tools to enhance cell growth in tissue
CC culture, increase the efficiency of gene transfer and help provide
CC more stable transformations. The proteins can be used as targets
CC to facilitate design and/or identification of inhibitors of those

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CC enzymes that may be useful as herbicides.
XX
SQ Sequence 1932 BP; 409 A; 548 C; 633 G; 337 T; 5 other;

alignment_scores:
Quality: 531.50 Length: 293
Ratio: 2.726 Gaps: 8
Percent Similarity: 66.553 Percent Identity: 42.321

alignment_block:
US-09-530-209a-2 x AAZ19961 ..
Align seg 1/1 to: AAZ19961 from: 1 to: 1932

42 GluSerGluGluIleIleMetGluMetValGluLysGluLysGlnHisLe 58
:::|||||:::
443 CAGTCGAGAGAAATGCGTGGCGGCTGTGTGAGCGGGGAACGGGACCAAT 492
58 uproSerAspAspTyrIleLysArgLeuArgSerGlyAspLeuAspLeu 75
:::|||||:::
493 GCCGGGCGCTGCTACGGCGACAGGCTGCGGGCGGCGGCGGCTGTCTT 542
75 snValGlyArgArgAspAlaLeuAsnTrpIleTrpHisAlaCysGluVal 91
|||
543 GCCTC...CGCCGGAGAGCCGCTGACTGATTTGGAAAGCTTACAGCAC 589
92 HisGlnPheGlyProLeuLysPheCysPheCysLeuAlaMetAsnTyrLeuAsp 108
|||:::|||||
590 CACAGGTTCCGCCCTCTCACTGCTTGTGAGTCACTTACCTCGATC 639
108 gphLeuSerValHisAspLeuProSerGlyLysGlyTyrPheGlnLeuGln 125
|||||
640 CTTCCTCTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 689
125 euleuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluIleThrGln 141
|||||
690 TCCTGCGGCGTGGCGTGGCTTCTGTGCGCCCAAGATGAGAGAAACGCC 739
142 ValProMetLeuIleAspLeuGln...ValGlyAspProGlnPheVal 157
|||||
740 GTCCCGAGCTCGTGGAGCTTCACAGAGTTCGAGAGAGCGGAGTACGTGT 789
157 egluAlaLysSerValGlnArgMetGluLeuValLeuAsnLysLeu 174
|||||
790 CGAGCGCAAGACGCTCCAGAGATGAGAGTCTGTCTTAACAACCTCA 839
174 ystTrpArgLeuArgAlaIleThrProCysSerTyrIleArgTyrPheLeu 190
:::|||||
840 ACTGAGAGATGATGATGCGTGCAGCCGCTTCTCTACGTGATTAATCTCTG 889
191 ArgLysMetSerLys...CysAspGlnGluProSerAsnThrLeuIle 206
:::|||||
890 AACAGACTCAACACAGCGCGGACGCGCGCGGAGAGCTGTGCTCTT 939
206 rArgSerLeuGlnValIleAlaSerThrThrLysGlyIleAspPheLeu 223
:::|||||
940 GCATCTCCGCGGAGCTTATCTTGGTGGCGGACAGAGAACCGCTGCGTGC 989
223 IupHepProSerGluAlaAlaAlaAlaValAlaLeuSerValSerGly 239
|||||
990 GGTTCAGCGCTCCGAGATCGCGCGGTTTCAGAGCGGCGTGGCGGA 1039
240 GluLeuGlnArg.....ValHisPheAs 247
:::|||||
1040 GAGCGGAGCAGCGGAGCGGCTGACAGACCGCTGCTGCTACAGAGA 1089
247 PAsnSerSerPheSerProLeuPheSerLeuGlnLysGluArgVal 263
|
1090 T.....AAGAGCGCGGT 1103
264 .....LysLysIleGlyLeuMetIleGluSerAspGlySerAsp 276
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1104 TGGCGTCCAGGAAGCGATCGGTCATGGCTCTCCGGCGGCATTGAC 1153
277 LeucySer..... 279
1154 GAGCTACCTGTCACCGAATCTCGAGAGCGAGCTCCCGCTGCC 1203
280GlnThrProAsnGlyValLeuGluValSerAlaCysCyspHis 294
1204 CGTCCCGCAGCGCTGTGGGGTCTGGAC...GCCGCTCCCTGCTCA 1250
294 erpHelysThrhAspSerSerSerSer 303
1251 GCTACAGAGCGAAGCGCGACTCGG 1279
seq_name: /SID2/gcgcdata/geneseq/geneseqn/NA2000.DAT: AAC42423
seq_documentation_block:
ID AAC42423 standard; DNA; 1337 BP.
XX AAC42423;
AC
XX
DT 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 35500.
DE
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
XX EPI03405-A2.
XX
PD 06-SEP-2000.
XX
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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AC AAV33885;
XX
DT 25-JAN-1999 (first entry)
XX
XX N. tabacum CYCD3;1 gene.
DE
XX D-type cyclin; growth; plant; cell-division control; phosphorylation;
KW CDC; Rd; retinoblastoma; germination; flowering; seed; fruit;
KW root development; ds.
XX
XX Nicotiana tabacum.
OS
XX W09842851-A1.
XX
PD 01-OCT-1998.
XX
XX 24-MAR-1998; 98WO-EP01701.
XX
PR 26-MAR-1997; 97EP-0302096.
XX
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX Murray JAH;
XX
XX WPI; 1998-532012/45.
XX
XX
XX Regulating growth and structure of plants by modulating protein that
PT controls cell division - specifically a D-type cyclin, and related
PT chimeric genes and transformed cells and plants, used to alter
PT growth rate, flowering, seed production etc.
XX
XX
PS Claim 14; p54; 75pp; English.
XX
XX This sequence represents the CYCD3;1 cDNA from Nicotiana tabacum which
CC encodes a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.
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90 uValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyrLeuA 107
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seq_documentation_block:
; Sequence 3, Application US/08463772
; Patent No. 6066501

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GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: LAHVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1970 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 22..948
US-08-463-772-3

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Quality: 240.50 length: 298
Ratio: 1.286 gaps: 15
Percent Similarity: 62.752 Percent Identity: 29.530

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193 MetSerLysCysAspGIngluProSerAsnThrLeuIleSerArgSerIe 209
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seq.documentation.block:
Sequence 51, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESS: Seidel, Gonda, Lavoorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8363

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;
; TELEFAX: (215)568-5549
;
; TELEX: NO. 5734038
;
; INFORMATION FOR SEQ ID NO: 51:
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; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 1325 base pairs
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; TYPE: nucleic acid
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; STRANDEDNESS: single
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; TOPOLOGY: linear
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US-08-306-691B-51

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679 CGCAACAACGCGCAACCTTGGTGGCTTGTGGCCACAGATGTGAAGTT 728

Page 6

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ADDRESS: Leona L. Lauder
STREET: Stewart Street Tower, 18th Fl., One Market
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,893A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,120
FILING DATE: 17-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-210-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 142..1026
US-08-472-893A-7

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seq_documentation_block:
; Sequence 7, Application US/08947492
; Patent No. 6127118
; GENERAL INFORMATION:
; APPLICANT: Meeker, Timothy C.
; TITLE OF INVENTION: BCI-1 Locus Nucleic Acid Probes and
; NUMBER OF INVENTIONS: Assay Methods
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: Stewart Street Tower, 18th Fl., One Market
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/947,492
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/472,893
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lauder, Leona L.
 REGISTRATION NUMBER: 30,863
 REFERENCE/DOCKET NUMBER: 91-210-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-777-9257
 TELEFAX: 415-543-4219
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4221 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 142..1026
 US-08-947-492-7

alignment_scores:
 Quality: 236.00 Length: 293
 Ratio: 1.349 Gaps: 13
 Percent Similarity: 59.727 Percent Identity: 28.669

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seq_documentation_block:

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? Sequence 1, Application US/08460694
? Patent No. 5858655
? GENERAL INFORMATION:
? APPLICANT: Arnold, Andrew
? TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
? STREET: 1100 New York Avenue, N.W., Suite 600
? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/460,694
? FILING DATE: 02-JUN-1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: McConathy, Evelyn H.
? REGISTRATION NUMBER: 35,279
? REFERENCE/DOCKET NUMBER: 0609.4070002
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-371-2540
? TELEFAX: 202-371-2540
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4244 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single

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TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 148..1035
 US-08-460-694-1

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 Quality: 236.00 Length: 293
 Ratio: 1.349 Gaps: 13
 Percent Similarity: 59.727 Percent Identity: 28.669

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Sequence 1, Application US/08460744
Patent No. 6107341
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609,4070005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 148..1035
US-08-460-744-1
  
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Quality: 236.00 Length: 293
 Ratio: 1.349 Gaps: 13
 Percent Similarity: 59.727 Percent Identity: 28.669

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Align seg 1/1 to: US-08-460-744-1 from: 1 to: 4244

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400  CTGACCGCTTCTCTGTGCTGGAGACCCGTGAAGAAAGACC... 441
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122  eLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGln 139
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442  .CTGCAGCTGCTGGGGCCACTTCATCATGTCGTGGCCCTTAAGATGAAG 490
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139  InThrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe 155
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156  ValPheGlnAlaLysSerValGln.....ArgMetGluLeu 167
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523  ATCTACACCCACAACATCTCATCCGCCCGAGAGAGCTGCTGCAATATGAGCT 572
      .....: ||||| ||||| .....:
167  uLeuValLeuAsnLysLeuIleuSTrParGLeuArgAlaIleThrProCys 184
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184  eTyrIleArgTrpPheLeuArgLysMetSerLysCysAspGlnGluPro 200
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623  ATTTCATGTGAACCTCTCTCCAAATAGCCA.....GAGCGGAGAG 666
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201  SerAsnThrLeuIleSerArgSerLeuGlnVal...IleAlaSerThr 216
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seq_documentation_block:
  Sequence 4, Application us/08770761A
  Patent No. 5814503
  GENERAL INFORMATION:
    APPLICANT: Kovacevic, Steven
    APPLICANT: Otto, Keith A.
    APPLICANT: Rao, Rameshchandra N.
    TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
    TITLE OF INVENTION: REGULATORY PROTEINS
    NUMBER OF SEQUENCES: 8
    CORRESPONDENCE ADDRESSES:
      ADDRESSEE: Eli Lilly and Company
      STREET: Lilly Corporate Center/Patent Division
      CITY: Indianapolis
      STATE: IN
      COUNTRY: USA
      ZIP: 46285
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk

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1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: Patent In Release #1.0, Version #1.30
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US-
6  FILING DATE: 19-DEC-1996
7  CLASSIFICATION: 530
8  ATTORNEY/AGENT INFORMATION:
9  NAME: Gaylo, Paul J.
10 REGISTRATION NUMBER: 36,808
11 REFERENCE/DOCKET NUMBER: X-10136
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 317-376-0756
14 TELEFAX: 317-277-1917
15 INFORMATION FOR SEQ ID NO: 4:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 4453 base pairs
18 TYPE: nucleic acid
19 STRANDEDNESS: single
20 TOPOLOGY: linear
21 MOLECULE TYPE: cDNA
22
23 US-08-770-761A-4

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[illegible]

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2875 AACAAACAGATCATCCGCAACACGCGACACCTTCCTGCTCTGTGTC 2924
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; Patent No. 5814503
; GENERAL INFORMATION:
; APPLICANT: Kovacevic, Steven
; APPLICANT: Otto, Keith A.
; APPLICANT: Rao, Ramachandra N.
; TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770.761A
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-376-0756
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-770-761A-6

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  ratio: 1.349        gaps: 13
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2514 GCGGTCCATG.....CGAAGATCGTCCGACCTGACCTGATGAGTGT 2557
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seq_documentation_block:
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: Patent No. 5988582
: GENERAL INFORMATION:
: APPLICANT: BEACH, David H.
: TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII(text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/246,361A
: FILING DATE: 19-MAY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/963,308
: FILING DATE: 16-OCT-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/888,178
: FILING DATE: 26-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/701,514
: FILING DATE: 16-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Matthew P. Vincent
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MIT-004C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1911 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 22..888
: US-08-246-361A-3

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Ratio: 1.323 Percent Identity: 29.153
Percent Similarity: 60.339

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256 CTGGCCATGATTTACTTGCAGCCGTTTCTTGCT....GGGCTCCGAC 299
117 rGlyLysGlyTyrPleLeuGlnLeuLeuAlaValAlaCysLeuSerLeuA 134
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Date: Jan 21, 2002 1:18 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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Search information block:

Query: US-09-530-209a-2
Database: ESTs
Database sequences: 11351937
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DEFINITION tomato shoot/meristem Lycopersicon esculentum cDNA clone
C70F24H8 5' sequence, mRNA sequence.
ACCESSION BG129531
VERSION BG129531.1 GI:12629719
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 673)
AUTHORS van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
TITLE Generation of ESTs from tomato shoot/meristem tissue
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University,
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES

source

1. 673

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="C70F24H8"

/tissue_type="shoot/meristem"

/dev_stage="developing shoots from 4-6wks old plants"

/note="vector: pBluescript SK(-); site_1: EcoRI; site_2: XhoI; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."

BASE COUNT

201 a 89 c 158 g 225 t

ORIGIN

alignment_scores:

Quality: 630.50

Ratio: 3.542

Percent Similarity: 68.462

Percent Identity: 51.923

Length: 260

Gaps: 5

alignment_block:

US-09-530-209a-2 x BG129531

Align seg 1/1 to: BG129531 from: 1 to: 673

43 SercInGluUlleIleMetGluMetValGluLysGluLysGlnHisLeupr 59

30 AGTGAAGAAAGCTTCTCTGATTCGTAAGAAAGAAAGAAATGATTTTACC 79

59 oSerASPSPtyrIleLysArgLeuArgSerGlyAspLeuAspLeuAsnV 76

80 AAAGATGATTAATTCATTAAGATTAAGATTAAGATTAAGATTAAGAT 128

76 aLgIyArgAspAlaLeuAsnTriplerLysAlaGlyValHis 92

129 .CATGAAGAAAGCTGTTAATTCGTAAGAAAGCTCATGTCATTAT 176

93 GlnPheGlyProLeuGlyPheGlyLeuAlaMetAsnTyrLeuAspArgph 109


```

258 CTTTCCTGATCTTCTTTGAATCAACGAT...GATCAAGTCCA 304
      ::::: ||||| ::::: |||||
201 SerAsnThrLeuIleSerArgSerLeuGlnValIleAlaSerThrIly 217
      ::::: || ||||| ::::: |||||
305 TTAAGCTTCAATTAATGATGATCCAACTATATATGAGCACTGCAAG 354
217 SGVILLeaSPheLeuGlnPheArgProSerGluAlaIleAlaVala 234
      ::||| ::||| ::||| ::||| ::||| ::|||
355 AGGATGACTCTCTTGAAATTTAAACCATGAGATTGACAGCACTGG 404
234 ILeuSerValSerGlyGlnLeuGlnArgVal..HisPheAspAsnSer 250
      ::||| ::||| ::||| ::||| ::||| ::|||
405 CTATGATGATGATGCGGGAACCAACCACTGCACTGGGAAGCATG 454
250 erPheSerProLeuPheSerLeuLeuGlnLysGluArgValLysIle 266
      ::||| ::||| ::||| ::||| ::||| ::|||
455 TCTGTTCT.....GATTCACACAGCTAGATA 480
267 GYGLuMetIleGluSerAspGlySerAspLysSerGlnThrProAs 283
      ||||| ||||| ::||| ::||| ::||| ::|||
481 GGAGAGACTTTGAA.....GTGTTTCAATGATCCGAG 515
283 ngIyValLeuGlnValSerAlaCys 291
      ::||| ::||| ::|||
516 AGGATGATGCAACAGTGCCTGC 540

```

seq_name: gb.escl:BE442681

seq_documentation_block:

LOCUS BE442681 621 bp mRNA EST 25-JUL-2000
DEFINITION WHE1101_A09_A17Zs wheat etiolated seedling root normalized cDNA
sequence.

ACCESSION BE442681 GI:9442114
VERSION BE442681
KEYWORDS
SOURCE bread wheat.

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.
1 (bases 1 to 621)

REFERENCE Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

TITLE The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)

JOURNAL Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

FEATURES
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
seq primer: Stralagene SK primer.
Location/Qualifiers

1..621
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1101_A09_A17"
/clone_lib="Wheat etiolated seedling root normalized cDNA
library"
/issue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda uni-ZAP XR, excised phagemid
pluscript SK; Site 1: EcoRI; Site 2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in

the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pluscript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

alignment_scores:
Quality: 468.00 Length: 209
Ratio: 3.059 Gaps: 4
Percent Similarity: 73.206 Percent Identity: 50.239

alignment_block:
US-09-530-209A-2 x BE442681 ..
Align seg 1/1 to: BE442681 from: 1 to: 621

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96 ProLeuCysPheCysLeuAlaMetAsnTyrLeuAspArgPheLeuSerVa 112
      ||||| ::||| ::||| ::||| ::||| ::|||
112 IHisAspLeuProSerGlyLysGlyTyrPheLeuGlnLeuAlaVala 129
      ::||| ::||| ::||| ::||| ::||| ::|||
51 CTATCCCTTCCTGAGCAAAAGCTTGGGACACACCTTGGCACTGG 100
129 IAcysLeuSerLeuAlaAlaLysIleGluGlnPheGlnValPrometLeu 145
      ||||| ::||| ::||| ::||| ::||| ::|||
101 CTTCCTGCTCCCTCGCTTCAAGATGAGAGAGACTTGTGCCCTCCC 150
146 ILeaSPheLeuGlnValGlyAspProGlnPheValPheGlnAlaLysSerVa 162
      ::||| ::||| ::||| ::||| ::||| ::|||
151 GTGACCTGCGAGGTGTTGAGGCAAAATTCGCTTCAGGGAAGACCAT 200
162 IGlutArgMetGluLeuValLeuAsnLysLeuLysTyrPheGlnArgVa 179
      ::||| ::||| ::||| ::||| ::||| ::|||
201 AAAAAGATGAGAGCTTGTGCTCACACCACTTAAATGAGGATGCAAG 250
179 IAlaThrProCysSerTyrIleArgTyrPheLeuArgLysMetSerLys 195
      ::||| ::||| ::||| ::||| ::||| ::|||
251 CTGTTACTGCTGCTCATTTATTCACACTTCCGCGCAATTCATGAT 300
196 CysAspGlnGluProSerAsnThrLeuIleSerArgSerLeuGlnVal 212
      ::||| ::||| ::||| ::||| ::||| ::|||
301 CATGAC...GCGCCCTCCATGCTGCTCCGCTTCGACCGACCAT 347
212 eAlaSerThrLysGlyIleAspPheLeuGlnPheArgProSerLys 229
      ::||| ::||| ::||| ::||| ::||| ::|||
348 CCTGAGCAGACAGCTAAAGACCTGATTTTGTGTTGACACTTCAAGA 397
229 IAlaIleAlaValAlaLeuSerValSerGlyGlnLeuGlnArgValHis 245
      ::||| ::||| ::||| ::||| ::||| ::|||
398 TTGCTGCAAGTGTGCACTTGCCCATTTGGGAGCCCAATTCATGATA 447
246 PheAspAsnSerPheSerProLeuPheSerLeuLeuGlnLysGluArg 262
      ::||| ::||| ::||| ::||| ::||| ::|||
448 GTGACGCGGGGTACACTACTTGCACATTC.....ATTAACAAGAGCG 491
262 gValLysLysIleGlyLysMetIleGlu..... 271
      ::||| ::||| ::||| ::||| ::||| ::|||
492 AGTGTTAAGATGCTACGATTTGATTAAGAACATAGCAATGGGAACA 541
272 .....SerAspGlySerAspLysSer.....GlnThrPro 282
      ||| ||||| ::||| ::||| ::||| ::|||

```

```

542 TTGCTTAAAGTCAGCTGATCATCATGTTCTGTGCGCAAGCCCG 591
283 AsnGlyValLeuGluValSerAlaCys 291
      |||||.....
592 ATATGCTGTGGATGCTGCTGCATGT 618
seq_name: gb_est2:B1306295

seq_documentation_block:
LOCUS      B1306295          790 bp      mRNA          EST          20-JUL-2001
DEFINITION NL_4_B12 Drought stress (leaf) Oryza sativa cDNA clone NL_4_B12 3',
            mRNA sequence.
ACCESSION  B1306295
VERSION    B1306295.1 GI:14981617
KEYWORDS   EST.
SOURCE     Oryza sativa.
            Oryza sativa.
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 790)
AUTHORS   Reddy,A.R., Ramakrishna,M., Chandrasekhar,A., Nagabhusan,I.,
            Ravindrababu,P. and Bennetzen,J.L.
            Novel EST enrichment with normalized cDNA libraries from drought
            stressed rice (Oryza sativa L.cv Nagina 22)
            Unpublished (2001)
JOURNAL    Contact: Reddy AR
            Department of Plant Sciences, School of Life Sciences
            University of Hyderabad
            P.O. Central University, Hyderabad-500 046, A.P, India
            Tel: 0091-40-3010265
            Fax: 0091-40-3010145
            Email: arjuls@uohyd.ernet.in
            Insert Length: 790 Std Error: 0.00
            Plate: 4 row: B column: 12
FEATURES   Seq primer: GTAAACGACGCGCACGTG.
            Location/Qualifiers
            source          1..790
                        /organism="Oryza sativa"
                        /cultivar="Nagina 22 (indica sub sp)"
                        /db_xref="taxon:4530"
                        /clone="NL_4_B12"
                        /clone_lib="Drought stress (leaf)"
                        /tissue_type="Entire leaf tissue"
                        /dev_stage="35 day-old seedlings"
                        /note="Organ: leaf; Vector: T7T3pac; ESTs from normalized
                        leaf cDNA library from drought stressed seedlings"
BASE COUNT      222 a      239 c      179 g      150 t
ORIGIN
align_scores:
      Quality: 443.00      Length: 185
      Ratio: 3.120      Gaps: 2
      Percent Similarity: 76.757      Percent Identity: 48.649

alignment_block:
US-09-530-209A-2 x B1306295/rev ..

Align seg 1/1 to reverse of: B1306295 from: 1 to: 790

```

```

92 HIsGlnPheGlyProLeuCySpheCysLeuAlaMetAsnTyrLeuAsp 108
      ::::::::::::::::::::
449 TACAACTTTGACCACTGACCTTACCTCGCAGTGAAGTACTGATAG 400
108 gPheLeuSerValHisAspLeuProSerGlyTyrGlyTyrPheLeuGln 125
      |||||.....
399 GTTCCTCTCTCTCTTAAATCTCCCTCATGACGAATCTTGATGCACACGT 350
125 euleuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluGlu 141
      |||||.....
349 TGCTGTACATAGTACTATCTCTGCTGACGAAGATGAGAGACCGTG 300
142 ValProMetLeuIleAspLeuGluValGlyAspProGlnPheValPheG 158
      |||||.....
299 GTCCCTCTTCCCATGACCTTCAGGTTTGTGATGCGGAATATGTGTGA 250
158 uAlaLysSerValGlnArgMetGluLeuValLeuAsnLysLeuLysT 175
      |||||.....
249 AGCAGGCATATTAAAGATGAGATGAGCTTATGTGATGAAGAACCTGAAT 200
175 rPArgLeuAlaGAlaIleThrProCysSeryTyrIleArgTyrPheLeuArg 191
      |||||.....
199 GGAGGCTGCAGAGCTGTGACCCCATCTCTTTCATFCGCTACTCTTGAC 150
192 LysMetSeryLysCysAspGlnGluProSerAsnThrLeuIleSerArgSe 208
      |||||.....
149 AAGTTCAATGAA...GGGAAAGCCCGAGCTACACGCTGCATCATAGTGC 103
208 rLeuGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheA 225
      ::::::::::::
102 CTCGATCTCAGTACAGTGGCAGCTCTGAAGAGCTAGTCTTGTCTCATTTCA 53
225 rGrPro 226
      |||||
52 GACCT 48
seq_name: gb_est2:BG585146

seq_documentation_block:
LOCUS      BG585146          809 bp      mRNA          EST          11-APR-2001
DEFINITION EST186909 MHAM Medicago truncatula/Glomus versiforme mixed EST
            library cDNA clone PMHAM-22A23 5' end, mRNA sequence.
ACCESSION  BG585146
VERSION    BG585146.1 GI:13600210
KEYWORDS   EST.
SOURCE     Medicago truncatula/Glomus versiforme mixed EST library.
            Medicago truncatula/Glomus versiforme mixed EST library
            Eukaryota; mixed EST libraries.
REFERENCE  1 (bases 1 to 809)
AUTHORS   Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Uterback,T., Cho,J.
            and Fraser,C.M.
            ESTs from roots of Medicago truncatula after colonization with
            Glomus versiforme, 2001
            Unpublished (2001)
JOURNAL    Contact: Harrison M.J.
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73401
            Tel: 580-223-5810
            Fax: 580-221-7380
            Email: mjharrison@noble.org
            Noble EST name: N380619e TIGR sequence name: MWDCA127K More
            information is available at: http://www.medicago.org
            Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
FEATURES   Location/Qualifiers
            source          1..809
                        /organism="Medicago truncatula/Glomus versiforme mixed EST
                        library"
                        /cultivar="Medicago truncatula genotype A17"
                        /db_xref="taxon:119092"
                        /clone="PMHAM-22A23"
                        /clone_lib="MHAM"
                        /tissue_type="roots colonized with Glomus versiforme"

```

/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
 /lab_host="E. coli strain XL0LR"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the UniZap XR vector from StrataGene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in XL0LR cells."

BASE COUNT 194 a 196 c 173 g 246 t
 ORIGIN

alignment_scores:

Quality: 428.00 Length: 256
 Ratio: 2.474 Caps: 6
 Percent Similarity: 67.578 Percent Identity: 38.672

alignment_block:

US-09-530-209a-2 x BG585146 ..

Align seg 1/1 to: BG585146 from: 1 to: 809

```

7  GLeuSerLeuLeuGlyThrGluSerAsnValAspAspGluGlyMetI 23
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
31  GACTGCGACCTCTCTCGCGGAG.....GACTCGCGGAGCTCTCT 71
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
23  eValAspGluThrProIleGluIleSer.....::: 32
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
72  CACCGGAGATTACG...GAATGCTCTCCGACCTGCATTCATTCAT 118
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
33  .....IleProGluMetGlyPheSerGlnSerGluSerGluGly 46
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
119  CATCGCAGTGGCGCGTCGTCATTTATTCGCCGAGAGAGAGAGAGTCG 168
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
47  IleMetGluMetValGluGlyGlnHisLeuProSerAspSply 63
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
169  ATTGCTGTTTTCATCGACGAGTTCAAGTTGTTCTGTTTCGACTA 218
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
63  rIleLysArgLeuArgSerGlyAspLeuAsnValGlyArgArg 80
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
219  CGTCTCAAGTTTCCATTCCTCGCTCTCGAATCCACACC...AGAGA 265
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
80  sPaLeuAsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyPro 96
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
266  AACCCATTGCATGATTCACAGCTACATGATATGATTTTCAGCCG 315
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
97  LeuGlyPheCysLeuAlaMetAsnTrpLeuAspArgPheLeuSerVal 113
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
316  TTTACGCGCTACCTCTCGTTACTATATGATCGGTTTTCGATCTCTC 365
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
113  sAspLeuProSerGlyLysGlyTrpIleLeuGlnLeuAlaValAlaC 130
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
366  ACCTTTACCGGAATCAATGATGCGCACTGCACATTTTATCTGTTCAT 415
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
130  yLsLeuSerLeuAlaAlaLysIleGluGluThrGluValPrometLeu 146
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
416  GTTTCCTTACGACGAGAAGATGAGAGAACCACTGCTCTCTCTCTTA 465
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
147  AspLeuGlnValGlyAspProGlnPheValPheGluAlaLysSerVal 163
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
466  GACTTTCAGTTGAGCTGCCAATATCATTTTCAACCAAGAGAGATTC 515
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
163  nArGmetGluLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAla 180
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
516  TAGAATGAGACTCTGTTCTGCTGCTATTTTGATTTGAGGCTGATCAA 565
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
180  leThrProCysSerTrpIleArgTrpPheLeuArgLysMetSerLysCys 196
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

566  TCACCCCACTTAGTTTCCTCAGTTTCTT.....CGCTGC 600
197  AspGluGluProSerAsnThr.....LeuIleSerArgSerIle 209
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
601  AACCTAGATTCACTGAGACTTTACACCACTTCATATTTTCACGTCCTAC 650
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
209  uGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArg 226
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
651  AGAATCATCTTATCTATATATCCAGATGCTACTTCTTACTTACAGGC 700
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
226  roSerGluAlaAlaAlaValAlaLeuSerValSerGlyGluGln 242
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
701  CATCATGATTCCTGCTGCAGCTCATCTCTGACGATATGAAATTCCT 750
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
243  ArgValHisPheAspAsn 248
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
751  AATTGCTCTTTTCTTAAAT 768
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|

```

seq_name: gb_est2:BG646052

seq_documentation_block: 810 bp mRNA

LOCUS BG646052 EST 24-APR-2001
 DEFINITION EST507671 KV3 Medicago truncatula cDNA clone PKV3-48G20 5' end,
 mRNA sequence.

ACCESSION BG646052

VERSION BG646052.1 GI:13781164

KEYWORDS EST.

SOURCE

ORGANISM

Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.

REFERENCE 1 (bases 1 to 810)

AUTHORS Vandenbosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Bowman
 C.L., Craven,M.B., Cho,J. and Fraser,C.M.

TITLE

ESTs from roots of Medicago truncatula 72 h after Rhizobium
 inoculation, 2001

JOURNAL

Unpublished (2001)

CONTACT: Vandenbosch K
 Department of Biology
 Texas A&M University
 College Station, TX 77843-3258, USA

Tel: 409 845 7707
 Fax: 409 845 2891
 Email: kate@mail.bio.tamu.edu

M394459e TIGR sequence name: MTECU46TK More information is
 available at: www.medicago.org

Seq primer: SKmod (CTA GAA CTA
 Location/Qualifiers

FEATURES

SOURCE

1..810

/organism="Medicago truncatula"

/cultivar="genotype A17"

/db_xref="taxon:3880"

/clone="PKV3-48G20"

/clone_lib="KV3"

/tissue_type="Seedling roots"

/dev_stage="3 days post-inoculation with Sinorhizobium
 meliloti"

/lab_host="E. coli strain XL0LR"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
 was directionally ligated into the UniZap XR vector from
 StrataGene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-zap phage using Ex-assist
 helper phage and propagated in XL0LR cells."

BASE COUNT 195 a 201 c 170 g 244 t

ORIGIN

alignment_scores: Quality: 426.50 Length: 266

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1 MetAlaGluGlnAsnLeu..... 6
111 ||||| |||||
34 ATGATTGAAAGAGCAATTCGCCGCAATTCATCCATCCACCTCCAGACACCTC 83
7 GluLeuSerLeuLeuLeuLeuLeuSerLeuSerLeuValAspAspGluGlyMetI 23
||||| ||||| ||||| ||||| |||||
84 CGACTCGGACCTCTCTCGCGGGAG..... GACTCGTCGAGAGTCC 124
23 LeuValAspGluThrProIleGluIleSer..... 32
||||| ||||| |||||
125 TCACCGGAGATTATACCG...GAATGCTCTCCGACCTGGATTCATCATCA 171
33 ..... IleProGlnMetGlyPheSerGlnSerGlnSerGluGluI 46
||||| ||||| ||||| ||||| |||||
172 TCATCGGAGTTGGCGCTGCTGCTATTATTGGCAGAGAAAGAGAGGAGTTC 221
46 eIleMetGluMetValGluLeuGluGlnHisLeuProSerAspAspT 63
||||| ||||| ||||| ||||| |||||
222 GATTGCTGTTTATCATCGACGACAGTTCAGTTGTTGCTCGGTTTGACT 271
63 yrlleLysATGLeuATGSerGlyAspLeuAspLeuValGlyATGATG 79
||||| ||||| ||||| ||||| |||||
272 ACGCTCAAGATTCATATCCGCTCTCTCGAATCCAGACAC...AGAGAA 318
80 AspAlaLeuAsnThrIleThrPlyLysAlaGluValHisGlnPheGlyPr 96
||||| ||||| ||||| ||||| |||||
319 GAACCCATGTGATGATTCATCAAGTACATGATGATATGATTTGATTCAGCC 368
96 oLeuGlyPheGlyCysLeuAlaMetAsnTyrlleuAspArgPheLeuSerValH 113
||||| ||||| ||||| ||||| |||||
369 GTTATACGCGCTACTCCCGTTTACCTATATGATGATGGTTTGGATTCTC 418
113 IsAspLeuProSerGlyGlyGlyTyrlleuGlnLeuLeuAlaValAla 129
||||| ||||| ||||| ||||| |||||
419 GACCTTACCGGAAATCAATGATGATGCCACTGCACACTTTATCTGTTGCA 468
130 CysLeuSerLeuAlaAlaTyrlleuGluGluThrGluValProMetLeuI 146
||||| ||||| ||||| ||||| |||||
469 TGTTTGCTTTAGACGAAAGATGAGAGAACCACTGTTCTCTCTCT 518
146 eAspLeuGlnValGlyAspProGlnPheValPheGluAlaLysSerValG 163
||||| ||||| ||||| ||||| |||||
519 AGACTTTCAGATTTAGAGTGGCCAAATTCATATTTTCAACCAAGGCGATTC 568
163 LncArgMetGluLeuValLeuAsnLysLeuTyrlleuAspLeuAlaValAla 179
||||| ||||| ||||| ||||| |||||
569 TTAGAATGAGACTGCTGTTCTGACTATTTGGATTTGGAGGCTGAGTCA 618
180 IleThrProCysSerTyrlleuArgTyrlleuValArgLysMetSerLysCy 196
||||| ||||| ||||| ||||| |||||
619 ATCACCACCATGATTCTCTCAGTTCTTT.....GCGTGG 653
196 sAspGlnIleuProSerAsnThr.....LeuIleSerArgSerL 209
||||| ||||| ||||| ||||| |||||
654 CAAGCTAATATCAATCGAATTCACCACTTCATATTTTCAAGCTGCTCA 703
209 eugInValIleAlaSerThrThrTyrlleuGlyIleAspPheLeuGluPheArg 222
||||| ||||| ||||| ||||| |||||
704 CAGAATATCTTATCTATATATCAAGATGCTAGCTTTCTTACTTACAGG 755
226 ProSerGluAlaAlaAlaValAlaLeuSerValSerGlyLeu 241
||||| ||||| ||||| ||||| |||||
754 CCATCATGCAATTCGCGAGCTGCATATCTCTGAGAGCTATGAATT 801

```

seq. documentation block: 775 bp mRNA EST 24-APR-2001
LOCUS BG645553 EST5071712 KW3 Medicago truncatula CDNA clone pKW3-46J23 5' end,
DEFINITION mRNA sequence.
ACCESSION BG645553
VERSION BG645553.1 GI:13780665
SOURCE EST.
ORGANISM Medicago truncatula
barrel medic.
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Eukaryota: Viridiplantae: Magnoliophyta: eudicotyledons: core eudicots:
Spermatophyta: Rosidae: eucosids I; Fabales; Fabaceae: Papilionoideae: Trifolieae:
Medicago.
1 (bases 1 to 775)
VandenBosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Bowman
,C.L., Craven,M.B., Cho,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula 72 h after Rhizobium
inoculation, 2001
Unpublished (2001)
Contact: VandenBosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel.: 409 845 7707
Fax: 409 845 2891
Email: kate@tamu.edu
M33960e TIGR sequence name: MTECC60TK More information is
available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA gtc gat CC).
FEATURES
source I..775
Location/Qualifiers

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/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV3-46J23"
/clone_id="KV3"
/tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
melliotti"
/lab_host="E. coli strain XL0LR"
/note="Vector: phuescript SK -; Site.1: EcoRI; Site.2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phase using Ex-assist
helper phage and propagated in XL0LR cells."
BASE COUNT      183 a      185 c      167 g      240 t
ORIGIN

alignment_scores:
    Quality: 423.00      Length: 253
    Ratio: 2.431      Gaps: 6
Percent Similarity: 68.775      Percent Identity: 39.130

alignment_block:
US-09-530-209A-2 x BG645553      ..

Align seg 1/1 to: BG645553 from: 1 to: 775

7 GluDeuserLeuEncysThrGluSerAsnValAspAsp..... 19
::: ::||| ||| |||::: ||
4 GACTGCGAGCTCCTCTGCGGGAGAGACCTGTCGAGAGTCCACCGAG 53
::: |||::: ||| :::::
20 ...GluGlyMetLeuVal Asp...GluThrProLeuGluIleSerIle 33
||| |||::: ||| :::::
54 ATTACCGGATGCTCTCCGACCTGGATTCATCATCATCATGCACTTG 103
|||::: ::::: ||| |||
34 ProGlnMetGlyPheSerGlnSerGlnGluIleLeuMetGluMet 50
|||::: ::::: ||| |||
104 CCGTCGTCGTCATTATTTGCCCGAGAGAGAGAGAGCATGCTGCTTTT 153

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```

50 tValGluLySGluLySGlnHisLeuProSerAspTyrIleLeuArgL 67
   ::::: ||| ::::: ::::: ||| ::::: ||| ::::: |||
154 CAtCGAGCAGCACTTCAAGTTTGTCTGCTTGCATGCTCTCAAGAT 203
   ::::: ||| ::::: ||| ::::: ||| ::::: |||
67 euArGSerGlyAspLeuAspLeuAsnValGlyArgAspAlaLeuAsn 83
   ::::: ||| ::::: ||| ::::: ||| ::::: |||
204 TCAATCTGCTCTCTCGAATCCAGACC...AGAGAAAGACCATTCGA 230
   ::::: ||| ::::: ||| ::::: ||| ::::: |||
84 TrpIleTrpValAlaCysGluValHisGlnPheGlyProLeuGlyPheCys 100
   ||||| ::::: ||| ::::: ||| |||||
251 TGGATTCTCAAGGTACATGATGATGATTTGATTCGACCTTTACCGG 300
   ||||| ::::: ||| ::::: ||| |||||
100 sleuAlaMetAsnTyrLeuAspArgPheLeuSerValHisAspLeuPro 117
   ||||| ::::: ||| ::::: ||| |||||
301 CCTCTCGCTTAACTATATGATGATGATTTGATTCGACCTTTACCGG 350
   ||||| ::::: ||| ::::: ||| |||||
117 erGlyLySGlyTrpIleLeuGlnLeuAlaValAlaCysLeuSerLeu 133
   ::::: ||| ::::: ||| ::::: ||| ::::: |||
351 AATCAATATGATGATGATGATGATTTTATCTGCTGATGCTTCTTTA 400
   ::::: ||| ::::: ||| ::::: ||| ::::: |||
134 AlaAlaLySLeuGluGluThrGluValProMetLeuIleAspLeuGluVal 150
   ||||| ::::: ||| ::::: ||| |||||
401 GCAGCAAGATGAGAGAACCACTGTTCTCTCTTACACTTCAGAT 450
   ||||| ::::: ||| ::::: ||| |||||
150 lGlyAspProGlnPheValPheGluAlaLySValGlnArgMetGluL 167
   ||||| ::::: ||| ::::: ||| |||||
451 TGAAGTGCCTCAATATATGATGATGATTTTATCTGCTGATGATGAGC 500
   ||||| ::::: ||| ::::: ||| |||||
167 euLeuValLeuAsnLySLeuLySTrpArgLeuArgAlaIleThrProCys 183
   ||||| ::::: ||| ::::: ||| |||||
501 TGTCTTGTCTGACTATTTTGTGATGAGGCTGATGATCAATCACCACCT 550
   ||||| ::::: ||| ::::: ||| |||||
184 SerTyrIleArgTyrPheLeuArgLySMetSerLySAspGlnLupr 200
   ||||| ::::: ||| ::::: ||| |||||
551 AGTTTCTCTGATTTCTTT...GCATGCAAGCTAGATTC 585
   ||||| ::::: ||| ::::: ||| |||||
200 oSerAsnThr...LeuIleSerArgSerLeuGlnValIleA 213
   ||||| ::::: ||| ::::: ||| |||||
586 AACTGGAACCTTCAACCCACTTCAATATTCAGCTGCTACGAATCATCT 635
   ||||| ::::: ||| ::::: ||| |||||
213 lAserThrThrLySGlyIleAspPheLeuGlnPheArgProSerGluAla 229
   ||||| ::::: ||| ::::: ||| |||||
636 TATCTAATATTCAGAGATGCTAGCTTCTTCTTACAGGCCATCATGAT 685
   ||||| ::::: ||| ::::: ||| |||||
230 AlaAlaValAlaLeuSerValSerGlyGluLeuGlnArgValHisPh 246
   ||||| ::::: ||| ::::: ||| |||||
686 GCTGCAAGCTGCTACTCTCTGAGCTAATGAATTCCTAATTTGCTCTT 735
   ||||| ::::: ||| ::::: ||| |||||
246 eaSAsn 248
   |||||
736 TGTTAAT 742
   |||||
seq_name: gb_est2:BG585934
seq_documentation_block:
LOCUS BG585934 834 bp mRNA EST 11-APR-2001
DEFINITION E1748769 MHAM Medicago truncatula/Glomus versiforme mixed EST
library cDNA clone PMHAM-31L19 5' end, mRNA sequence.
ACCESSION BG585934
VERSION BG585934.1 GI:1360098
KEYWORDS Medicago truncatula/Glomus versiforme mixed EST library.
SOURCE Medicago truncatula/Glomus versiforme mixed EST library.
ORGANISM Eukaryota; mixed EST libraries.
REFERENCE 1 (bases 1 to 834)
AUTHORS Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
and Fraser,C.M.
TITLE ESTs from roots of Medicago truncatula after colonization with
Glomus versiforme, 2001
JOURNAL Unpublished (2001)
COMMENT Contact: Harrison M.J.
Plant Biology Division

```

```

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N381409e TIGR sequence name: MTDCR707K More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA GAA CTA gta gAT CC).

FEATURES
    source
        1..834
            /organism="Medicago truncatula/Glomus versiforme mixed EST
            library"
            /cultivar="Medicago truncatula genotype A17"
            /db_xref="taxon:119092"
            /clone="PMHAM-31L19"
            /clone_1lb="MHAM"
            /tissue_type="roots colonized with Glomus versiforme"
            /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
            post-inoculation with Glomus versiforme. The library was
            made from a mixture of RNA from each of these stages."
            /lab_host="E. coli strain XL0LR"
            /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
            XhoI; cDNA was prepared from polyA+ enriched RNA from
            roots harvested at 10, 17, 22, 31 and 38 days
            post-inoculation with Glomus versiforme. The cDNA was
            directionally ligated into the Unizap XR vector from
            Stragene and packaged using Gigapack III Gold packaging
            extracts. Plasmids containing cDNA inserts were excised
            from the recombinant lambda-Zap phage using Ex-assist
            helper phage and propagated in XL0LR cells."

BASE COUNT      198 a      205 c      176 g      255 t
ORIGIN

alignment_scores:
    Quality: 422.50      Length: 266
    Ratio: 2.414      Gaps: 7
    Percent Similarity: 65.789      Percent Identity: 37.594

alignment_block:
US-09-530-209A-2 x BG585934
Align seg 1/1 to: BG585934 from: 1 to: 834

1 MetAlaGluGluAsnLeu..... 6
   ||| ||||| ::::: |||
32 ATGATTGAAAGCAATTCATGCGCAATTCATGCGCACTGTCACACCTC 81
   ::::: ||| ::::: ||| ::::: |||
7 GluLeuSerLeuLeuGlyThrGluSerAsnValAspAspGluGlyMetI 23
   ::::: ||| ::::: ||| ::::: |||
82 CGACTGCGAGCTCTCTGCGGGAG.....GACTCGTGGAGGTCC 122
   ||||| ::::: ||| ::::: ||| |||||
23 lValAspGluThrProIleGluIleSer..... 32
   ::::: ||| ::::: ||| |||||
123 TCACCGGAGATTTACCG...GAATGCTCTCCGACCTCGATTCATCATCA 169
   ::::: ||| ::::: ||| |||||
33 .....lIleProGlnMetGlyPheSerGlnSerGluSerGluIle 46
   ::::: ||| ::::: ||| ::::: ||| |||||
170 TCATTCGCGAGTTGCCGCTGCTCATTTATTCGCCGAGAGAGGAGATC 219
   ::::: ||| ::::: ||| ::::: ||| |||||
46 eIleMetGluMetValGluLySGluLySGlnHisLeuProSerAspSPT 63
   ||||| ::::: ||| ::::: ||| |||||
220 GATTGCTGTTTTCATCGACGACGAGTTCAAGTTTGTCTGCTTTCACCT 269
   ::::: ||| ::::: ||| ::::: ||| |||||
63 lTyrIleLySArgLeuArgSerGlyAspLeuAsnValGlyArgArg 79
   ||||| ::::: ||| ::::: ||| |||||
270 ACGCTCAAGATTCATTCATTCGCTCTCGAATCCAGCACC...AGAGAA 316
   ::::: ||| ::::: ||| ::::: ||| |||||
80 AspAlaLeuAsnTrpIleTrpValAlaCysGluValHisGlnPheGlyPr 96
   ::::: ||| ::::: ||| ::::: ||| |||||
317 GAAGCCATGATGATGATTCCAAGTACATGATGATTTGATTTGAGCTTCA 366
   ::::: ||| ::::: ||| ::::: ||| |||||
96 oLeuGlyPheCysLeuAlaMetAsnTyrLeuAspArgPheLeuSerValH 113

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111 |||
367 GTTAACGGCGTACCTCCGTTAACTATATGATCGTTTGGATTCTC 416
113 isaspleuproserglylytrpilleuglnleuvala129
417 GACCTTACCGGAATCAATGATGGCACTGCACCTTTATCTGTTGCA 466
130 CysleuSerleuAlaAlaLysIleGluGluThrGluValPrometleu1146
467 TGTGTGCTTACGACCAAGATGAGAGACCACTGCTCTCTCTCTT 516
146 eaapleuglnvalgllyasproglinphevalphegluAlaLysSerValG 163
517 AGACTTTCATATTGAAGTGCACCAATACATATTTCAACAGAGCATTC 566
163 InArgmetGluLeuValLeuAlaLysLeuLysLeuLysTrpArgLeuArgAla 179
567 TTGAGATGAGAGCTGCTGTTCTGACTATTTGGATTGGAGCTGAGATCA 616
180 IleThrProCysSerTyrlleArgTyrPheLeuArgLysMetSerLysCy 196
617 ATCACCCTAGTAGTTCTCAGCTTCTT.....GCGTG 651
196 saspglnglnProSerAsnThr.....LeuIleSerArgSerL 209
652 CAAGCTGATGCAACTGGAAGTTCACCCACTTCATATTTTCACGTGCTA 701
209 euGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArg 225
702 CAGAAATCATCTTATCTAATATCCAGATGCTAGCTTTCTTACTTAAGG 751
226 ProSerGluAlaAlaAlaValAlaLeuSerValSerGlyGluLeu 241
752 CCATCATGATTCATGCTGACGCTGCATCTCTGACACTAATGAATTT 799

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seq_name: gb_est1:BE642779

seq_documentation_block:

LOCUS BE642779 813 bp mRNA EST 01-SEP-2000
 DEFINITION Cri2_6_P20.SP6 Ceratopteris Spore Library Ceratopteris richardii
 CDNA clone Cri2_6_P20 5', mRNA sequence.

ACCESSION BE642779
 BE642779.1 GI:9960458

VERSION BE642779.1 GI:9960458

KEYWORDS EST.

SOURCE Ceratopteris richardii.

ORGANISM Ceratopteris richardii.

REFERENCE 1 (bases 1 to 813)

AUTHORS Chatterjee,A., San Miguel,P., Stout,S.C., Banks,J. and Roux,S.J.

TITLE Expressed sequence tags of cDNA clones from a C. richardii library

JOURNAL Unpublished (2000)

COMMENT Section of Molecular Cell and Developmental Biology

University of Texas

Biology Building, Room 16, Austin, TX 78712, USA

Tel: 512 471 4238

Fax: 512 232 3402

Email: sroux@uts.cc.utexas.edu

Plate: Cri2_6 row: P column: 20

Seq primer: SP6.

FEATURES

source

1. 813

Location/Qualifiers

/organism="Ceratopteris richardii"

/cultivar="Brogn"

/db_xref="taxon:49495"

/clone="Cri2_6_P20"

/clone_lib="Ceratopteris Spore Library"

/tissue_type="gametophyte"

/cell_type="Spore"

/dev_stage="20 hours after germination initiation"

/note="Vector: PCWSPORT6; EST sequence from cDNA library.

cDNA library constructed from mRNA isolated from C.

richardii spores that had developed for 20 hours after their germination had been initiated by white light."

alignment_scores:

Quality: 401.50 Length: 241
 Ratio: 2.419 Gaps: 5
 Percent Similarity: 68.880 Percent Identity: 40.249

alignment_block:

US-09-530-209a-2 x BE642779

Align seg 1/1 to: BE642779 from: 1 to: 813

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78 ArgArgspAlaLeuAsnTrpIleTrpLysAlaCysGluValHisGlnph 94
111 |||
10 CGGACAGAGGCGCATTCAGCTGATTTCTAAGCTTCGAGATTCTACATTT 59
94 egIlyProLeuCysPheCysLeuAlaMetAsnTyrLeuAspArgPheLeu 111
60 TGGCGCTTTGACTGTGGCGCTCTGTGAACTACGTTGATGATTCCTTT 109
111 ervaHisAspleuproserglylysglytrpilleuglnleuvala 127
110 CTGTGCAAAAGATCCGCGTGAAGAACCGTGATGATGATGATGCTATGTC 159
128 ValAlaCysLeuSerleuAlaAlaLysIleGluGluThrGluValProm 144
160 GTGGCATGATTCATTCATTCGCTGCAAAATGAGAAAGATGAGAGTGGCT 209
144 tLeuIleAspleuglnValAlaLysProGlnPheValPheGluAlaLys 161
210 ATTGCTGAGACTTCAGGTT...GATCCAGAGTGTGTTTGAACCTCGGA 256
161 ervaGlnArgMetGluLeuValLeuAlaLysLeuLysLeuLysTrpArg 177
257 CAATTCACGATGAGAACTGCTGCTGAGCACTTTCGATGAGCAATG 306
178 ArgAlaIleThrProCysSerTyrlleArgTyrPheLeuArgLysMetSe 194
307 AGTTCGTGACACCATTTGCTTATATAGACTGCTTAAGATCAATTTGA 356
194 rLysCysAspGlnGluProSerAsnThrLeuIleSerArgSerleuGln 211
357 C...CTGATTCGACGCTTCATTCGCTCTCTCTCCGCTGCTACAGC 403
211 alIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArgProSer 227
404 TTATTTTGTGCGCTATTCAGAGACTTAATTTCTCTCTTCGCGGCATCT 453
228 GluAlaAlaAlaValAlaLeuSerValSerGlyLys.....Le 241
454 GCCATTCGCTGTCATTCATTCGTCGTCGTCGTCGTCGTCGTCGTCAT 503
241 uGlnArgValHisPheAspAsnSerSerPheSerProLeu..... 254
504 GGAACCTTACTAACTTAAGGGAGCTTATTCCTGTATTTAGTTGACAGT 553
255 .....PheSerleuLeuGlnLysGluArgVal 263
554 TGCAAGATACATGTGAAGATGCTTTACCTCGCTGTCGACAGATATACAA 603
264 LysLysIleGlyGluMetIleGluSerAspGlySerAspLysSer.. 279
604 TTGCACCATTTACATGATGTCAGATGAATAATATATTTTGTGACAGC 653
280 GlnThrProAsnGlyValLeuGluValSerAlaCysCysPheSerPheL 296
654 TAGACGCGCTATGCGAGTGTGATGCTTCATTTAGTTGACAGTGA 703
296 yThrHisAspSerSerSer 303

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704 GCACATTGAAGTCAGCGGCTCT 726

seq_name: gb_est2:BG726093

seq_documentation_block:

LOCUS BG726093 498 bp mRNA EST 09-MAY-2001
DEFINITION sae06b09.y1 Gm-cl055 glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl055-4578 5' similar to TR:Q9ZRX9 Q9ZRX9 CYCLIN D2.1
PROTEIN: mRNA sequence.

ACCESSION BG726093 GI:14011162

VERSION EST

KEYWORDS

SOURCE

ORGANISM

glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
glycine.
1 (bases 1 to 498)

REFERENCE

AUTHORS

Shoemaker, R., Keim, P., Vockin, L., Erpeiding, J., Coryell, V., Khanna,
'A., Bolla, B., Matz, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,
'Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Allevy, N., Schurr,
'R., Ratter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,
'R., Waterston, R. and Wilson, R.
Public Soybean EST Project

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 412.
Location/Qualifiers

FEATURES

source

1..498
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl055-4578"
/clone_11b="Gm-cl055"
/tissue_type="Mature seed pods, greenhouse grown"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI. The cDNA library was constructed from mRNA isolated
from mature seed pods of greenhouse grown plants prior to
senescence for the cultivar KPI. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."

BASE COUNT 136 a 83 c 107 g 172 t

ORIGIN

alignment_scores:

Quality: 385.00

Ratio: 3.500

Percent Similarity: 68.750

Length: 160

Gaps: 4

Percent Identity: 49.375

US-09-530-209a-2 x BG726093

Align seg 1/1 to: BG726093 from: 1 to: 498

72 LeuAspLeuAsnVa1G1yArGaSPaLaLeuAsnTrp11eTrpLysAl 88
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3 TTGGACTTGGAGTCTT...ACGAAGAGAGGCTCTGATGGATTGGGAAGGC 49
88 acyGluValHnISlOpheG1yProLeuCySPheCyLeuAlaMetLysT 105
1 TCATGCATCTTGGACTTGGACCTGTACCTTATGCTATGCTGTTACT 99
50 TCATGCATCTTGGACTTGGACCTGTACCTTATGCTATGCTGTTACT 99
105 yrlLeuAspArpHeLeuSerValHnISasPheuProSerG1yLysG1yTrp 121
|||||
100 ACTTGATCGGTCCTATCATGATATGATATGATATGATATGATATGATATG 149
122 TleuG1nLeuAlaVala1aCySLeuSerLeuAla1aLys11eG1 138
|||||
150 AGTATGCACCTGTAGCTGTAGCTGTAGCTGTAGCTGTAGCTGTAGCTGA 159
138 uG1uThrGluValProMetLeuLeuAspLeu.Gln..... 149
200 GGAAGATTAAAGTCTCTCTGTGTAGATTACAGATTAGTGTAGATCTTA 249
149 149
250 CTACCCAGATTTGCAATATATCTTTGGGTGGCATCTACATTTCTCTC 299
150ValGlyAspProGlnPheV 156
300 TGATTTTATCATCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 349
156 alPheG1uAlaLysSerValG1nArGmetG1uLeuValLeuAsnLys 172
350 CATTTGAGCTAAAGACATTCAGATGAGATGAGATGAGATGAGATGAGACA 399
173 LeuLysTrpArpLeuArGa1a1eThrProCySerTyrlLeuArgTyrrp 189
400 TTGAGATGAGAAATGCAAGCTTCACATTCATTCCTCTCTAGATTACTT 449
189 eLeuArG1yMetSerLysCySasPglN 198
450 CCTCAGAGAGATCATCT...TGTGACCAA 474

seq_name: gb_est1:A1728767

seq_documentation_block:

LOCUS A1728767 512 bp mRNA EST 11-JUN-1999
DEFINITION BNLGH11561 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (AJ011692) cyclin D2.1 protein [Nicotiana tabacum], mRNA
sequence.

ACCESSION

A1728767

VERSION

A1728767.1

GI:5047619

KEYWORDS

EST.

SOURCE

upland cotton.

ORGANISM

Gossypium hirsutum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

REFERENCE

1 (bases 1 to 512)

AUTHORS

Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.

TITLE

ESTs from developing cotton fiber

JOURNAL

Unpublished (1999)

COMMENT

Contact: Ben Burr

Biology Department

Brookhaven National Laboratory

Upton, NY 11973, USA

Tel: 516-344-3396

Fax: 516-344-3407

Email: burr@bnl.bnl.gov

Seq primer: T3 primer.

Location/Qualifiers

1..512

/organism="Gossypium hirsutum"

FEATURES

source

1..512

/organism="Gossypium hirsutum"

/cultivar="Acala Maxxa"
 /db_xref="taxon:3635"
 /clone_lib="Six-day Cotton fiber"
 /tissue_type="Immature fiber"
 /dev_stage="Six days post anthesis"
 /lab_host="XLI-Blue"
 /note="Vector: pBluescript II KS+"
 BASE COUNT 146 a 86 c 113 g 167 t
 ORIGIN

alignment_scores:

Quality: 369.50 Length: 172
 Ratio: 3.213 Gaps: 7
 Percent similarity: 66.860 Percent identity: 49.419

alignment_block:

US-09-530-209a-2 x AT728767 ..

Align seg 1/1 to: AT728767 from: 1 to: 512

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4  GUAsnleuGluLeuSer.....LeuLeuGysThrGlu..... 14
   ::::::::::: ||| |||||::: |||
3  AAAAATCTGATGTTTCACCCCTCAAACTCTCTCTGTGAGAGACGCAAG 52
   |||
15 .SerAsnValAspAspGlu.....GlyM 22
   |||
53 TCTCTGCTTGATGATGATCTGATTTTATGCCATTAAGAGAGTTGGGG 102
   |||
22 erileValasp.....Glu 26
   :: |||
103 TTTCCTCCCTGATGTGACCAACCACTTAAACCAAACTTTATACACAA 152
   |||
27 ThrProleGluLeuSer.....IleProGluMetGlu 37
   |||
153 GACCCCTTTTCATTAACACAGATCACTATTGATGGGTGAGTCTGG 202
   |||
37 yPheSerGlnSerGluSerGluGluIleIleMetGluMetValGluysG 54
   |||
203 TTTTCCA...ATACAAAGTATGATGCAATCAAGAGATGCTGTAAGAA 249
   |||
54 IuLysGlnHisLeuProSerAspArgTyrIleLysArgLeuArgSerGly 70
   |||
250 AGGTGAGACATTTGGCTGAAGATGATTAATCTCAAGAGACTGAGAAAGTGG 299
   |||
71 AspleuAspleuAsnValGlyArgAspAlaLeuAsnTyrIleTyrPly 87
   |||
300 GATTTGGCTTGAGTGT...ACGAAAGAGGCTCTGATTGATTGGA 346
   |||
87 salAcysGluValHisGlnPheGlyProLeuGysPheCysLeuAlaMet 104
   |||
347 GGCCTTCGCTTATTACGTTTGGACCTTGGACCTTGGCTTATCCATTA 396
   |||
104 snTyrLeuAspArgPheLeuSerValHisAspleuProSerGlyLysGly 120
   |||
397 ACTACTTGATCGGCTTCTTACGTTATGACTTACTTACAGGTAACA 446
   |||
121 TrrPleleuGlnleuAlaValAlaCysLeuSerLeuAlaLysIle 137
   |||
447 TGGACCTGCAATTTGCTGTGCTTTGTTTATCAATGACGCAAAAT 496
   |||
137 egluGluThrGluVal 142
   |||
497 GAGAGAGACAAAGTT 512

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seq_name: gb_est1:AW042725

seq_documentation_block:

LOCUS AW042725 596 bp mRNA EST 18-SEP-1999
 DEFINITION ST24F07 Pine triplex shoot tip library Pinus taeda cDNA clone
 ACCESSION AW042725
 VERSION AW042725.1 GI:5903254

KEYWORDS

EST.
 lobliolly pine.
 SOURCE
 Pinus taeda
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 REFERENCE
 1 (bases 1 to 596)
 Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R.
 TITLE
 The Pine Gene Discovery Project
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Ross Whetten
 Forest Biotechnology Group
 North Carolina State University
 Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
 , NC, 27695-8008
 Tel: 919-515-7800
 Fax: 919-515-7801
 Email: rosswhetten@ncsu.edu
 Seq primer: 5' lambda triplex2 Sequencing primer.
 Location/Qualifiers

FEATURES

source

1..596
 /organism="Pinus taeda"
 /db_xref="taxon:3352"
 /clone="ST24F07"
 /clone_lib="Pine Triplex shoot tip library"
 /lab_host="E. coli BM25.8"
 /note="Organ: shoot tips; Vector: Lambda Triplex; Site:1:
 Sfil (A); Site:2: Sfil (B); Shoot tips (approx. 2 cm from
 apex) were collected during the spring, frozen and used
 for mRNA isolation. The SMART-PCR method (Clontech) was
 used to prepare a library from 1 ug total RNA, using the
 Lambda Triplex vector. Plasmid subclones in pTriplex were
 recovered by cre-lox excision in E. coli strain BM25.8 and
 sequenced from the 5' end."

BASE COUNT 135 a 152 c 153 g 151 t 5 others
 ORIGIN

alignment_scores:

Quality: 366.50 Length: 200
 Ratio: 2.637 Gaps: 4
 Percent similarity: 69.500 Percent identity: 41.500

alignment_block:

US-09-530-209a-2 x AW042725 ..

Align seg 1/1 to: AW042725 from: 1 to: 596

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102 AlameLAsnTyrLeuAspArgPheLeuSerValHisAspleuProSerG 118
   ::::::::::: ||| |||||::: |||
10 TCTATAACTATCTGATCGGTTTCTGTCAGGAATCCACTACCGAAGC 59
   |||
118 yLysGlyTrrPleleuGlnleuAlaValAlaCysLeuSerLeuAla 135
   |||
60 CAAGGCTGAGATGCGCAGCTCTATCTGTGGCTTGTCTCTGCTG 109
   |||
135 lalysIleGluGluThrGluValProMetLeuIleAspleuGlnValGly 151
   |||
110 CTAAATAGAGAGAAACCAAGTCTCTTACTCTGCACTTGCAGCGTGA 159
   |||
152 AspProGlnPheValPheGluAlaLysSerValGlnArgMetGluLeu 168
   |||
160 GAGCCGCACTCTCTTGCAGCCCGTACTATCCAAAGATGAGAGCTTCT 209
   |||
168 uValleuAsnLysLeuYstrPArgLeuArgAlaIleThrProCysSer 185
   |||
210 GGTTCGTGACACTCTGGAATGGCGGATCTCTCTTACACCGCTTTT 259
   |||
185 yTrleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluProser 201
   |||
260 TCTGCACTTACTTCTTCAGGCT...GAGGGGAGNAGGAGCCAGCGCG 306
   |||
202 AsnThrLeuIleSerArgSerLeuGlnValIleAlaSerThrThrLysG 218
   |||

```

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307 AGAGCTATGCTGGCGGACCAATGAGCTCATATTCACACACACACACT 356
218 yliaasppheleugluPheargProsergluAlaAlaAlaValAlaL 235
357 GTTGGATTCTTGAGACCGACCATCTGCATATGCTGCGAGCTGTAA 406
235 euserValserglyLueu.....GlnArgValHisPheasp 247
407 TCTGTCACTCGAGAGCTTTGCCCTCGAAGACGACGACAGAGAGAC 456
248 AsnSerSerPheSerProleu..... 254
457 CAT.....CCTGCTCTGCTCTCTGTAAAAAGATGGGTGT 494
255 .....PheSerleuLeuGlnLysGluArgValLysLysIleGlyGluM 269
495 CGGNTCCTATAGTCTGTATACAGAACTCTGATTGAGAAATTCGAGGCC 544
269 etlleuSerAspGlySerAspLeuCyserSerGlnThrProAsnGlyVal 285
545 TACAAAGAAATCAATCAATCCCTCATATCCGACANAGCCTGTTGGAGTG 594

seq_name: gb_est2:BG597062

seq_documentation_block:
LOCUS BG597062 728 bp mRNA EST 12-APR-2001
DEFINITION EST495740 csts Solanum tuberosum cDNA clone csts16p1 5' sequence,
ACCESSION BG597062
VERSION BG597062.1 GI:13615202.
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 728)
REFERENCE van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
AUTHORS Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
TITLE Generations of ESTs from sprouting potato eyes
JOURNAL Unpublished (2000)
COMMENT Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdaetesen.com
Seq primer: M13F-R.
FEATURES
source
Location/Qualifiers
1..728
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone_lib="csts"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/note="vector: pBluescript SK(+); Site1: EcoRI, Site2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."
BASE COUNT 183 a 178 c 144 g 223 t
ORIGIN

```

```

Align seg 1/1 to: BG597062 from: 1 to: 728
10 LeuLeuCyThrGlu.....SerAsnValAspAspG1 20
116 CTACTCTGCGGCGAGACCTCCGATACCGTTTCTCTCAACAGGAGAGAGA 165
20 uGlyMetIleValAspGluThrProIleGluIleSerIleProGluMetG 37
166 G.....GATTGCCGGAATGTT 182
37 LypheSerGlnSerGluSer.....GluGluIleIleMet 48
183 CCTCGTCGGATATCGAATCTCACTTCGCGCATATCGATGAATCAATCGCC 232
49 GluMetValGluLysGluLysGlnHisLeuProSerAspPryIlely 65
233 GGTCTTATCGAAGATGAAAGAAATTCGTACCTGATTGACTATATCGA 282
65 sArgLeuArgSerGlyAspLeuAspLeuAsnValGlyArgAspAlaL 82
283 GAATTCGAATCTCAATCTCTTAAGCGC...GCCGTAAGATGAATCCG 329
82 euAsnThrPileThrPlyAspAlaCysGluValHisGlnPheGlyProLeuCyS 98
330 TTGCATGAGATTCTCAAGGTACAGCGCACTATGTTTCCAGCCATTAAAG 379
99 PheCyLeuAlaMetAsnThrLeuAspArgPheLeuSerValHisAspLe 115
380 GCGTATCTCCGCGTTACTATTCGATCGTTTCTCTACTCGAGAAACCTT 429
115 uproSerGlyLysGlyThrPileLeuGlnLeuAlaValAlaCysLeuS 132
430 GCCGCAACAAATGCGCGCCACTTCACTATTTGCGTTGCTGCTAT 479
132 erLeuAlaAlaLysIleGluGluThrGluValProMetLeuIleAspLeu 148
480 CTTTACGTGCAAAAATGAGAGAACCTCTGTCTCTCTCTTTGATCTT 529
149 GlnValGlyAspProGlnPheValPheGluAlaLysSerValGlnArgMe 165
530 CAGTTTCAAGGTGCGAAGTATATTTGAACCAAAACTATCCAAAGAT 579
165 tGluLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIlehrp 182
580 GGAGTTTCTTGTGCTGAGATTTAGATTGAGCGCTCCGATTAACCTC 629
182 rCySserTrpIleArgTrpPheLeuArgLysMetSerLysCysAspGln 198
630 CGTTTACCTTCCTCAGCTTCTTTCACCTTAACCTGATTCACATAGAACT 679
199 GluProSerAsnThrLeuIleSerArgSerLeuGlnValIle 212
680 TTCACCTGCT...TTCCTTATCTCAAGGCTTTCACATTAATC 718

seq_name: gb_est1:AI728683

seq_documentation_block:
LOCUS AI728683 562 bp mRNA EST 11-JUN-1999
DEFINITION BNLH111316 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (A0101892) cyclin D2.1 protein [Nicotiana tabacum], mRNA
sequence.
ACCESSION AI728683
VERSION AI728683.1 GI:5047535
KEYWORDS EST.
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 562)
AUTHORS Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
TITLE ESTs from developing cotton fiber

```

JOURNAL Unpublished (1999)
 COMMENT Contact: Ben Burr
 Biology Department
 Brookhaven National Laboratory
 Upton, NY 11973, USA
 Tel: 516-344-3396
 Fax: 516-344-3407
 Email: burr@bnl.gov
 Seq primer: T3 Primer.

FEATURES
 source Location/Qualifiers
 1..562
 /organism="Gossypium hirsutum"
 /cultivar="Acala Maxxa"
 /db_xref="taxon:3635"
 /clone_lib="Six-day Cotton fiber"
 /tissue_type="immature fiber"
 /dev_stage="Six days post anthesis"
 /lab_host="XLI-Blue"
 /note="Vector: pBluescript II KS+"
 BASE COUNT 156 a 101 c 117 g 186 t 2 others
 ORIGIN

alignment_scores: Quality: 362.50 Length: 175
 Ratio: 3.208 Gaps: 5
 Percent Similarity: 64.571 Percent Identity: 44.571

alignment_block:
 US-09-530-209A-2 x A1728683 ..

Align seg 1/1 to: A1728683 from: 1 to: 562

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4  GluAnleuGluLeuSer.....LeuLeuGlyThrGluSer....15
   |||||.....|
44  GAAATCTGACTGTTCAACCTCAATCTTCTGTTCTGAGACACAG 93
15  .....15
94  CTTCTGCTTGATGATGATCTGATTTAATGCTTGAACGAGTTGGGG 143
16  .....AsnValasp 18
144  CTTCCCGTCCTTGTCATCACTTTAAAAACCAATCTTTAATCAAT 193
19  AspGluGlyMetIleValAspGluThrProIleGluIleSerIleProG1 35
   |||.....|
194  GACCCCTTCTTAATAACAAGATCACTCTTGTGATGGTGTGCT.. 241
35  nmetGlyPheSerGlnSerGlnSerGluGluIleIleMetGluMetValG 52
   |||||.....|
242  ....GTTTTGCA...TTACAAAGTATGATGATTAATTAAGCAATGGTTG 284
52  LuysGluGlyGlnHisLeuProSerAspAspTyrIleLysArgLeuArg 68
285  AAAAAGAGATGAGCATTTTGCCAGAGATGATTATCTTAAGAGACTGAGA 334
69  SerGlyAspLeuAspLeuAsnValGlyArgArgAspAlaLeuAsnTrp11 85
   |||||.....|
335  AGGGGAGATTGGAGTTGAGC...GCCAGAGAGAGCTAATGAATGGAT 381
85  eTrpLysAlaCysGluValHisGlnPheGlyProLeuGlyPheCysLeuA 102
   |||||.....|
382  TTGGAGCTTCANCTTATTCAATTTTGACCTGTGAGCTTTGGCTAT 431
102  labelAsnTyrLeuAspArgPheLeuSerValHisAspLeuProSerGly 118
   |||||.....|
432  CCATTAATCTACTGATCGGTCTCTCAATCATATGATTTACTAGAGGT 481
119  LysGlyTrpIleLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAla1 135
   |||.....|
482  AAAACATGAGACTGTCCAACTGTGGCGCTTGACATGTTATCTATTGACAN 531

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135 alysIleGluGluThrGluValPro 143
 :|||:|||||:|||||:
 532 TAAATGAGAGAAACAAAGTGCT 556

seq_name: gb_EST:BG886881

seq_documentation_block: 749 bp mRNA EST 30-MAY-2001
 LOCUS BG886881
 DEFINITION EST512732 cSTD Solanum tuberosum cDNA clone cSTD214 5' sequence.
 mRNA sequence.
 BG886881

ACCESSION BG886881.1 GI:14263967

VERSION EST.

KEYWORDS

SOURCE

ORGANISM Solanum tuberosum
 potatato.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 749)
 van der Hoeven, R., Bezzerides, J., Ewing, E., Cho, J., Chlemingo, A.,
 Bougri, O., Buell, C. R., Ronning, C., Tanksley, S. and Baker, B.

REFERENCE

AUTHORS

TITLE

JOURNAL

Unpublished (2001)

CONTACT: Cathy Ronning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries

Division tel 1-800-711-6195, email cda@resgen.com

Seq primer: M13p-R.

FEATURES

source

Location/Qualifiers

1..749

/organism="Solanum tuberosum"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="cSTD214"

/clone_lib="cSTD"

/tissue_type="dormant tuber"

/dev_stage="one month post-harvest"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; This library targets genes expressed in dormant
 tubers. This library was made from sections of dormant
 tuber, avoiding the buds and epidermis. Tubers were stored
 for one month post-harvest at 4°C. The tuber was peeled,
 well away from the surface. Then it was liquid nitrogen. This
 library is noted as p4 in Tanksley lab notebooks."

BASE COUNT 197 a 181 c 146 g 225 t

ORIGIN

alignment_scores: Quality: 360.00 Length: 187
 Ratio: 2.791 Gaps: 2
 Percent Similarity: 68.984 Percent Identity: 44.385

alignment_block:
 US-09-530-209A-2 x BG886881 ..

Align seg 1/1 to: BG886881 from: 1 to: 749

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78  ArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysGluValHisGlnP 94
   |||.....|
34  AGAGTGAATCGCTTGCAATGATCTCAAGTACACGACCATATGCTTT 83
94  eGlyProLeuGlyPheCysLeuAlaMetAsnTyrLeuAspArgPheLeu 111
   |||||.....|
84  CCAGCATTAACGGCGTATCTCGCCGTTAATTAATTTGATGATGTTCT 133
111  eValHisAspLeuProSerGlyLysGlyTrpIleLeuGlnLeuAla 127
   |||||.....|
134  ACTCGAAGACTTCCGCCAACAAATGCTGCGCCACTTCAACTATTTGCG 183
128  ValAlaCysLeuSerLeuAlaValAlaLysIleGluGluThrGluValPro 144

```

```
|||||
184 GTTGCTGCTTACTTACGACAAAATGAGAGACCTCTGTCTTC 233
144 tleuileaspleuGlnValGlyAspProGlnpheValpheGluAlaLys 161
234 CCTTGGATCTTCAGTGAAGCGCAAGATATATTTGAACCAAAAA 283
161 erValGlnArgMetGluLeuValLeuAsnLysLeuLysTrpArgLeu 177
284 CTATCCAAAGATGGAGTTCTTGTACTGAGCATATTAGATTGAGGCTC 333
178 ArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgLysMetSe 194
334 CGATCCATAACTCCGTTAGCTTCCTCAGTTCTTCCGCGTAACCTGA 383
194 rLysCysAspGlnGluProSerAsnThrLeuIleSerArgSerLeuGln 211
384 TTCACCTAGGAACTTTCACCTCG...GTCCCTATATCAAGCGCTTCTCAGA 430
211 aIleIleAserThrThrLysGlyIleAspPheLeuGlnPheArgProSer 227
431 TTATCTCTCTATATATTCAAGAACTAGCTTTCATGAGTATTGCCATCA 480
228 GluAlaIleAlaValAlaLeuSerValSerGlyGluLeuGlnArgVa 244
481 TGCATAGCTGCAGCTACATACTATGTGCAGCTAAGGACCTT..... 522
244 lHisPheAspAsnSerSerPheSerProLeuPheSerLeuLeuGlnLysG 261
523 .....CCAATTTCTCTCTTGTGATGCTG 547
261 LuArgValLys 264
548 AACATGCTGAA 558
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Db 121 TCTCCGTGTACACGCGAGCATCGCGGTGGAAATTGTGCGGAGAAATTCAGCAGGAGCG 180
QY 266 tcggaagacagtgctgttagtagacagcgagatctctcccggttagaagacagtg 325
Db 181 TCGGAGACGAGTGTCTGTATGACGACGCGGATTCCTCTCGGTTGAAGACAGTGT 240
QY 326 caaatcgaagaagaagatcgcgcgtgctgtgtgttctacatcgaagaagaatcga 385
Db 241 CAATCGAAGAAGAAATTCGTCGCTTGTGTCTGTCTACATCGGAGAGAAATCGAAA 300
QY 386 cggagaatcgaattgttagactcttgagaaataacgagtcgacatcgtgaacagaacg 445
Db 301 CGGAGAAATCGAATTTGTAGATCTTGAGAAATTAACGGTACGATCGTGAACAGAAACG 360
QY 446 tctgtgattacgagattgaaataagatgaggaatcgatgacatggaattctctcg 505
Db 361 TCGTGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 506 gtgagctgtgaagatgtagagtcgcgcgagtgtaagaaagatcgcagtgagcgag 565
Db 421 GTGCGCTGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 566 aaggaagctgagtagaagaatttttcaggtgagcgagaaagatcgcgaataagtg 625
Db 481 AAGGAAGCTGAGTTAGAACCTTTTTCAGGTGCGGAGAAAGATCTTGGAATTAAGTTG 540
QY 626 ttggaatgtctatgagataaactcgcgattcgaagaagaatgagccactgtgtgagga 685
Db 541 TTGGAATGTCTATGAGATTAACCTTCGATTCGAGAAAGATGAGCCTTGTTGAGGAG 600
QY 686 agatacagtgaggttaaatcgaatcgaagaagaagaatgagatgagatgagatg 745
Db 601 AGATACGATGGGTAAATTTGAATCCATGAGAGACGATGATGATGATGATGATGATG 660
QY 746 ttctcccaagactactatattttctctgtgaataactctgtctgattttctt 805
Db 661 TTTTTCACCAAGTACTTATTTATTTCTCTGTATTAATCTTTGATTTTCTTTT 720
QY 806 aacaaatccaaatgtagatatcttctctcgaataaataaataatgtaattcaactt 865
Db 721 AACCAATCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 866 ttgttactctctgagtgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatg 925
Db 781 TGTGTACTTCTCTGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
QY 926 agtta 931
Db 841 AGTTTA 846

RESULT 3
AX008796 755 bp DNA PAT 06-SEP-2000
LOCUS AX008796
DEFINITION Sequence 6 from Patent WO964599.
ACCESSION AX008796
VERSION AX008796.1 GI:9996260
KEYWORDS
SOURCE chae cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 755)
FOWLE, L. C., WANG, H. and CROSBY, W. L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 96/4599-A 6 16-DEC-1999;
FOWLE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASATCHEMAN TECHNOLOGIES (CA)
FEATURES
source 1.755
Location/Qualifiers
/organism="Arabidopsis thaliana"

BASE COUNT 229 a 106 c 187 g 233 t
ORIGIN
Query Match 79.9%; Score 744.8; DB 6; Length 755;
Best Local Similarity 99.7%; Pred. No. 1.8e-146;
Matches 746; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
/db_xref="taxon:3702"
QY 185 gtggaatctaggaataattctgtctccgtgtgtacagcgagaaatcgcggtggaattgt 244
Db 1 GTGGAATCTAGGATTAATTTCTGCTCCGTGTGTACAGCGCGAATGCGGTGAATTTGTG 60
QY 245 gggagaattcagcaagcgctgaggaagagtggttagtagtaagcgaggaattt 304
Db 61 GCGAATAATTCACAGAGCGCTGAGACGAGTGTGTATGATGATGATGATGATGATGATG 120
QY 305 cctccggttgaagaagatgctcaaatcgaagaagaatcgcggttctgtgtct 364
Db 121 CTTCCGCTTGAAGACAGTGTCAATCGAAGAAGATTCGCGGTTCTGCTTCT 180
QY 365 acatcggaagaagaatcgaagaagaaatcgaattgtgagatctgaggaataaagct 424
Db 181 ACATCGGAAGAGAAATCGAAGACGAGAAATCGAATTTGTAGATCTTGAGAAATTAACG 240
QY 425 gacgactgtgaagaacagaagaacgctgtgatttagagattgaaatgagtgaggaatc 484
Db 241 GACGATCGTCAAAACAGAAACGCTGTGATTTACGATGATTTGAATTAAGATGAGAAAT 300
QY 485 atgaacatggaattctctcgtgtgctgtgtgaagatgtagagtcgcgcgagttaaag 544
Db 301 ATGAACATGATTTCTTCTGCTGCTGCTTGAAGATGATGATGATGATGATGATGATG 360
QY 545 aagatctccatgagaacggtgagaagagctgagctgagaaatttttcaggtgagcgag 604
Db 361 AAGATCTCCATGAGACGAGGAGAAAGCTGATGAAACCTTTTTCAGTGTGCGGAG 420
QY 605 aagatctccgagaatagtggtgtgagatgtctatgagatgaatcgaattctcgaaga 664
Db 421 AAGATCTTCTGGAATGAATGTTGGAATGTTGATGAGATTAATTAATTAATTAATTA 480
QY 665 gatgagccactgtgtgaggaagatacgaatggtgttaatttgatccatgaagaagcga 724
Db 481 GATGAGCCACTTGTGTGAGAGAAATGAGATGAGATGAGATGAGATGAGATGAGATG 540
QY 725 tgaatgaatgaatgaatgttttcacaaagtaactaattttctctgtaaat 784
Db 541 TGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 785 ctgtgttgaattttctttaaacaataccaatgaaatgaaatccttctcgaataatc 844
Db 601 CTTTGTCTGATTTTCTTTTAACAAATCCAAATGATGATGATGATGATGATGATGATG 660
QY 845 aataacatgtaattcaactttgttgaatcctgtgagtgaaatgaatgagatcgtgt 904
Db 661 AATAACATGTAATTAACACTTTGTTGTACTTCTGAGGTAATTAATTAATTAATTAAT 720
QY 905 ttctcgaatgaataaactaagttat 932
Db 721 TTTCTCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 748

RESULT 4
ATT345 84196 bp DNA PLN 26-JAN-2000
LOCUS ATT345
DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone T345.
ACCESSION AL132979
VERSION AL132979.2 GI:6782244
KEYWORDS
SOURCE thae cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE
AUTHORS
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 84196)
Bloeker, H., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F. and
Salanoubat, M.
JOURNAL
Unpublished
2 (bases 1 to 84196)
EU Arabidopsis sequencing project.
REFERENCE
AUTHORS
Submitted (25-JAN-2000) MIPS, at the Max-planck-Institut fuer
Direct Submission
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
leemchemips.biochem.mpg.de, mayer@mps.biochem.mpg.de, Project
Coordinator: Marcel Salanoubat and Francis Quetier, Grouperment
d'Interet Public, Centre National de Sequencage - GENOSCOPE, 2 rue
Gaston Cremlieux, BP191, 91006 Evry Cedex, France;
http://www.genoscope.cns.fr
On Jan 27, 2000 this sequence version replaced gi:6434247.
COMMENT
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
FEATURES
source
1. 84196
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/note="similarity to predicted proteins, Arabidopsis
thaliana"

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/translation="MARLEHNSNGCARISPSNEFVEIRSEKSNKSNINISRSSES
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HPPPPPPQPDNDLNPITFKAIHDYAKPEKTPDLIRIKESVSESGDPIORGYPAE
ALSHKETESPSSSSSLEDFTILYFTLNDACTSKFAHITANQALILEATNOSNTHI
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TLFVLDWQOQNSIFSAODEAKFTFPMARHIMMDGEEETDQLKEIYFPGYVS
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intron
/number=5

[illegible][illegible]

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Db	547	TTTTTTTAACCTTTTACATATTATATTTTCAGGAATTAAGTTAATTTATTTGTGATTT	606
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Db	607	TGGAAATATTAAGA	619
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DEFINITION	Arabidopsis thaliana cyclin-dependent kinase inhibitor protein (ICK1) mRNA, complete cds.		
ACCESSION	U94772		
VERSION	U94772.1		
KEYWORDS	GI:2052501		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Wang, H., Fowke, L.C. and Crosby, W.L.		
AUTHORS	A plant cyclin-dependent kinase inhibitor gene		
TITLE	Nature 386 (6624), 451-452 (1997)		
JOURNAL	97242401		
FEATURES	2 (bases 1 to 856)		
TITLE	Wang, H., Fowke, L.C. and Crosby, W.L.		
JOURNAL	Direct Submission		
FEATURES	Submitted (20-MAR-1997) Plant Biotechnology Institute, 110		
TITLE	Gymnasium Place, Saskatoon, SK S7N 0W9, Canada		
FEATURES	Location/Qualifiers		
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BASE COUNT	292 a	92 c	225 g
ORIGIN	247 t		
Query Match	5.6%	Score 52.2;	DB 8; Length 856;
Best Local Similarity	56.5%;	Pred. No. 0.34;	
Matches 143; Conservative	0;	Mismatches 98;	Indels 12; Gaps 2;
Db	439	GAGATGCCAAGCGAATCGGAATTCGAAATTTTGTGGAGCTGAGAAACAACTCAAA	498
Qy	617	aataagttgttggaatgtctcatgaagataacttcgattcsgaagaatgagccactt	676
Db	499	GAAATTCAG-----AAGACGTCACATTTTCGATTCGACAGAGACAGCCATT	549
Qy	677	ggtgaggaagaacagatgggttaaatgtaacatcatgaagaagaacagatgataatga	736
Db	550	GA---AGGACGCTTACGATGGCTTAAGTTAGAGTGAAGAGCAACAGACGTTATGCTT	606
Qy	737	tgatcatgttttccaccaagactatattttctctgtaataatccttgcttgat	796

Db	607	TTTTTTTAACTTTTACGTTTAAATTTTACGGAATAAGTTAAATTTATTTTGTGTTGANT	666
QY	797	ttttctttaaca 809	
Db	667	TGGAATAATATAGA 679	
RESULT	9		
LOCUS	AX008791		
DEFINITION	Sequence 1 from Patent WO964599.	PAT	06-SEP-2000
ACCESSION	AX008791		
VERSION	AX008791.1	GI:9996255	
KEYWORDS			
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicts; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.		
REFERENCE	1 (bases 1 to 904) Fowke,L.C., Wang,H. and Crosby,W.L. Cyclin-dependent kinase inhibitors as plant growth regulators Patent: WO 964599-A 1 16-DEC-1999; FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV SASKATCHEWAN TECHNOLOGIES (CA) Location/Qualifiers 1..904		
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BASE COUNT	307 a 107 c 229 g 261 t		
ORIGIN			
Query Match	5.6%; Score 52.2; DB 6; Length 904;		
Best Local Similarity	56.5%; Pred. No. 0.34;		
Matches 143; Conservative	0; Mismatches 98; Indels 12; Gaps 2;		
QY	557	gagaaagcggaaagcgcgaagttaagaatttttcgcggtgcggagaagaattctcg 616	
Db	487	GAGAGCCACACGGAATCGAATTTAAAGCTTTTTTTGTGGAAAGTGGAACCAACTCAAA 546	
QY	617	ataagtcgttgaaagtctctaagaatataaacttcgaattcgaagaagatgaccact 676	
Db	547	GAATAATTCAG-----AAGAAGTACATTTTCGATTTGGAGAAGAGAAGCCATTAA 597	
QY	677	gttgaggaagatacgaatgggttaaatgaatccatgaagaagaacgaatgatgataatga 736	
Db	598	GA---AGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAAGAAAGAAAGTTATGTTT 654	
QY	737	tgatcatcgttttaaccacaaagtactatattttctctcgtgaataacttttgcttgat 796	
Db	655	TTTTTTTAACTTTTACGTTTAAATTTTACGGAATAAGTTAAATTTATTTTGTGATT 714	
QY	797	ttttctttaaca 809	
Db	715	TGGAATAATATAGA 727	
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DEFINITION	Sequence 22 from Patent WO0111061.	PAT	28-FEB-2001

[illegible]

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OY	908	cctgat	913
Db	824	VTTWWAY	829
RESULT	11		
LOCUS	AX008794		
DEFINITION	Sequence 4 from Patent WO964599.	PAT	06-SEP-2000
ACCESSION	AX008794		
VERSION	AX008794.1	GI:9996258	
KEYWORDS			
SOURCE	thalae cress.		
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi. 1 (bases 1 to 443)		
REFERENCE	Fowke,L.C., Wang,H. and Crosby,W.L. Cyclin-dependent kinase inhibitors as plant growth regulators Patent: WO 964599-A 4 16-DEC-1999;		
AUTHORS	POWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV SASKATCHEWAN TECHNOLOGIES (CA) Location/Qualifiers		
TITLE	1. .443 /organism="Arabidopsis thaliana" /db_xref="taxon:3702"		
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Db	206	GAGAGCCACGACGATCGGAATTGAAAGATTTTTTTGTGGAACTGAGAACAACACTCAA	265
OY	617	aataagttctggaatggtcatgaagataactcgatttcogaaagaatgagccact	676
Db	266	GAAATATTCAG-----AAGAGTAGTCAATTTTCGATTTCGAGAGAGAGCATTA	316
OY	677	ggtggaagaagaatgaggtgggttaaattgaatccatgaagaagaagatgatatga	736
Db	317	GA---AGACGCTTGAGATGAGTAAAGTTAGAGTAGAGAGAGAGAAAGTTATGCTTT	373
OY	737	tgatcatgttttcaccacaagacttatattttctctcgtataaaccttgtcttgat	796
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Db	434	T 434	
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LOCUS	AE001419	15892 bp DNA INV	06-NOV-1998
DEFINITION	Plasmidium falciiparum chromosome 2, section 56 of 73 of the complete sequence.		
ACCESSION	AE001419	AE001362	
VERSION	AE001419.1	GI:3845281	
KEYWORDS			
SOURCE	malaria parasite P. falciiparum.		
ORGANISM	Plasmodium falciiparum Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		

REFERENCE	1 (bases 1 to 15892)
AUTHORS	Gardner,M.J., Tetteelin,H., Carrucci,D.J., Cummings,L.M., Aravind,L., Koonin,E.V., Shallow,S., Mason,T., Yu,K., Fujii,C., Pederson,J., Shen,K., Jing,D., Aston,C., Lai,Z., Schwartz,D.C., Perea,M., Salzberg,S., Zhou,L., Sutton,G.G., Clayton,R., White,O., Smith,H.O., Fraser,C.M., Hoffman,S.L. et al.
TITLE	Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum
JOURNAL	Science 282 (5391), 1126-1132 (1998)
MEDLINE	99021743
REMARK	Erratum: [[published erratum appears in Science 1998 Dec 4;282(5393):1827]]
REFERENCE	2 (bases 1 to 15892)
AUTHORS	Gardner,M.J.
TITLE	Direct Submission
JOURNAL	Submitted (02-NOV-1998) The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, MD 20814, USA
FEATURES	Location/Qualifiers
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	/note="identified by sequence similarity; putative"
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[illegible]

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

HTG.
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 83365)
Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D.,
Fuji, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E.,
Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M.,
Koo, H., Morfitt, K.S., Cronin, L.A., Shen, M., Vanden, S.E., Umayam, L.,
Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H.,
Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D.,
Niemann, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and
Venter, J.C.
Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana
Nature 402 (6763), 761-768 (1999)
20083487
10617197
2 (bases 1 to 83365)
Lin, X.
Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:4587677.
The sequence and annotation of chromosome 2 were merged from those
of the individual clones on this chromosome after removing
overlaps. For detailed information, please see the TIGR web site
(http://www.tigr.org/tdb/at/at.html).

Genes were identified by a combination of three methods: Gene
prediction programs including GRAIL
(ftp://arthur.emm.ornl.gov/pub/grayail), GeneFinder (Phil Green,
University of Washington), Genscan (Chris Burge,
http://genome.stanford.edu/GENSCAN.html), and NetPlantGene
(http://www.cds.dtu.dk/services/NetGene2/), searches of the
complete sequence against a peptide database and plant EST
databases at TIGR, and manual curations based on those analyses.
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity are named as 'unknown' proteins.
Genes without protein or EST similarity, that are predicted by two
or more gene prediction programs over most of their length are
annotated as 'hypothetical' proteins. Genes encoding tRNAs are
predicted by tRNAscan-SE (Sean Eddy,
http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were
identified by RepeatMasker (Arian Smit,
http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
P6P23, P506, T17A5, and T1316, the ESSA group for sequencing clone
F1304, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards
and Satoshi Tabata for helpful assistance. In addition, we would
like to thank the TIGR Bioinformatics Department, especially Lixin
Zhou, Hanif Khalek, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy
Peterson, Michael Holmes, and Delwood Richardson for software and
database support.

This work was supported by the National Science Foundation,
Department of Energy and the US Department of Agriculture.

Address all correspondence to: atettigr.org.
Location/Qualifiers
1. 83365
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/cultivar="Columbia"
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/chromosome="II"
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NNSPPLRDPDLVGAMERKLELLCLDSCVEMIGTWPGGIGKTTIVFLNQLS
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SDALQIRCMYAFGQKPPYDGFYKLARKVTWVGNFPLGRVGSYFPEMSKOWRE
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LOCUS
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DEFINITION
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9 unordered pieces.
ACCESSION
AC016912
VERSION
AC016912.5 GI:15029483
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEPIN.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 213467)
AUTHORS
Waterston,R.H.
TITLE
The sequence of Homo sapiens clone
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 213467)
AUTHORS
Waterston,R.H.
TITLE
Direct Submission
COMMENT
Submitted (08-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jul 30, 2001 this sequence version replaced gi:14627163.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WTGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Center project name: H.NH0480A06
----- Project Information -----

----- Summary Statistics -----
Sequencing vector: M13, 338
Sequencing vector: plasmid, 358
Chemistry: Dye-Primer ET; 33% of reads
Chemistry: Dye-terminator Big Dye; 35% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 198028 bases at least Q40
Consensus quality: 200051 bases at least Q30
Consensus quality: 209092 bases at least Q20
Insert size: 19200; agarose-fp
Insert size: 211898; sum-of-contigs
Quality coverage: 7.79 in Q20 bases; sum-of-contigs
Quality coverage: 7.63 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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770
869: gap of unknown length
770
870 192693: contig of 191824 bp in length
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194176 194176: contig of 1383 bp in length
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FEATURES
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XX (CROP-) CROPDISEGN NV.
 PA De Almeida J, De Veylder L, Inze D, Landrieu I;
 XX WPI; 1999-229535/19.
 XX P-PSDB; AAW98179.
 DR
 XX DNA encoding inhibitor of cyclin-dependent kinase
 PS Claim 1b; Page 72-74; 88pp; English.
 XX
 CC This is the DNA sequence of FL39, a cDNA clone that encodes a new
 CC cyclin-dependent kinase (CDK) inhibitor (see AAW98179) of Arabidopsis
 CC thaliana. New plant products with a putative CDK inhibitory
 CC function were screened by using a two-hybrid system with CDC2at
 CC protein as bait and a library made from an RNA mixture of A.
 CC thaliana cell suspensions harvested at the early exponential,
 CC exponential, early stationary and stationary phases. Positive
 CC clones LDV39, LDV66 and LDV159 were obtained. Clone FL39 was
 CC isolated from a flower cDNA library using partial clone LDV39 as
 CC probe. Clone FL66 (see AAX25016) was similarly obtained using LDV66.
 CC Another CDK inhibitor, ALPCDK1 (see AAX25018), was obtained from
 CC alfalfa. Results established that several CDK inhibitors exist
 CC in plants and that these inhibitors are expressed at different
 CC time points and may have different functions during the development
 CC of the plant. CDK inhibitors, nucleic acids, antibodies, promoter
 CC sequences, related recombinant DNA and vectors are all useful: for
 CC diagnosis (no details); for modulating the cycle, division and/or
 CC growth of plant cells; for altering activity of CDK; for modulating
 CC growth inhibition in plants caused by environmental stress; for
 CC inducing male or female sterility; for altering cell division
 CC progression in plants, bacteria, fungi, insect and animal cells;
 CC and to screen for agonists or antagonists that are potentially
 CC useful as growth regulators or herbicides. Plants of any sort can
 CC be treated, e.g. to alter their size or resistance to disease.
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 XX Sequence 932 BP; 289 A; 125 C; 254 G; 264 T; 0 other;
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Query Match 100.0%; Score 932; DB 20; Length 932;
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 DT 18-OCT-2000 (first entry)
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 KW protein identification; signal transduction pathway;
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 OS Arabidopsis thaliana.
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AAC37798 AAC37798 standard; DNA; 886 BP.

AC AAC37798;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 18698.

XX Hybridisation assay; genetic mapping; gene expression control;

KM protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.
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Oy	469	taagagctgaagaaatccgaatgaaacatggaattctctctcgtgtgcgtgtbaaatgaaatc	528
Db	374	taagagctgaagaaatccgaatgaaacatggaattctctctcgtgtgcgtgtbaaatgaaatc	433
Oy	529	tgcgcgcaggttaaggaagagttccatggaacgctgaaagaagctgaagttagaagaattc	588
Db	434	tgcgcgcaggttaaggaagagttccatggaacgctgaaagaagctgaagttagaagaagattc	493
Oy	589	tttccaagctgcgcgaagaagaatcttcggaataagttgttgaaatgtctcgtgaagttaa	648
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Oy	649	cttcggaattccgaagaagaatgcagccacttgcgtggaagaagaatacagagctggttlaaatgaa	708
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Oy	769	ttctctctgtaataatcttttccttgaattttctctttaaaccnaatccaagtgaatattc	828
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XX	DE	Arabidopsis thaliana CDK inhibitor, ICK2 encoding cDNA.
XX	KM	Cyclin-dependent kinase inhibitor; CDK; Interactor of Cdc2 kinase 2;
XX	KM	ICK2; Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;
XX	KM	antisense construct; tissue-specific promoter; transgenic plant;
XX	KM	male sterility; ds.
XX	OS	Unidentified.
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XX	FT	/product= "ICK2"
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XX	PR	08-JUN-1998; 98CA-2235978.
XX	PR	31-DEC-1998; 98CA-2256121.
XX	PA	(MIAC) AGRIC & AGRIFOOD CANADA.
XX	PA	(UTSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX	PA	(CANA) NAT RES COUNCIL CANADA.
XX	PI	Wang H, Fowke LC, Crosby WL;
XX	DR	WPI: 2000-097540/08.
XX	P-PSDB:	AAV44336.

PT Modifying plant cell development using nucleic acid encoding inhibitor
 of cyclin-dependent kinase, or corresponding antisense sequence, e.g.
 PT for inducing male sterility -
 XX
 XX
 PS Disclosure; Fig 3; 58pp; English.
 XX
 CC The present sequence is a cDNA encoding ICK2 which inhibits A. thaliana
 CC Cyclin-Dependent kinase (CDK). Interactor of Cdc2 kinase 2 (ICK2)
 CC interacts with Cdc2c, D-class cyclins, Cyclo1, Cyclo2 and Cyclo3 and
 CC shares functional and sequence similarity with ICK1. Growth,
 CC morphogenesis, multiplication, enlargement, differentiation and
 CC maturation of plant cells can be modified by transforming them with
 CC nucleic acid encoding CDK inhibitor or antisense construct complementary
 CC to the inhibitor gene, operably linked to a tissue-specific promoter.
 CC The transgenic plants exhibit alteration of traits such as petals, male
 CC sterility and ability to set seeds.
 SO Sequence 755 BP; 229 A; 106 C; 187 G; 233 T; 0 other;

Query Match	79.9%	Score 744.8	DB 21	Length 755
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QY	245	gcgagaatctcgacgagcgctcggagacgagtgtgtatagatcagacgcgagattct	304	
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QY	305	cctccggtttgaagaacagtggtcaaatcgagaagaagaattcgtccggttcgtgttct	364	
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QY	365	acatcggaagagaatctcgaaacggaatcgaattctgaattcttgagagaaataacggt	424	
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QY	425	gacgatcgtgaaacagaaacgctcgtgattacgaatgatttgaataaagatvtggaatcg	484	
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DT 17-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
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PN EP1033405-A2.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147935.
PR 09-AUG-1999; 99US-0148171.
PR 10-AUG-1999; 99US-0148319.
PR 11-AUG-1999; 99US-0148341.
PR 12-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152263.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161820.
PR 28-OCT-1999; 99US-0161923.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 23.9%; Score 223; DB 21; Length 585;
Best Local Similarity 95.6%; Pred. No. 5e-42;
Matches 240; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
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QY 610 tcttcggaataagttgtgtaattctatgaagataacttcgatttcgagaagaatga 669
DB 335 tcaaggaataatgaagctgtgtaattctatgaagataacttcgatttcgagaagaatga 394
QY 670 gccacttggtgaggaagaacagagtggttaaatgaatccatgaagaagacgatgatg 729
DB 395 gccacttggtgaggaagaacagagtggttaaatgaatccatgaagaagacgatgatg 454
```

```
QY 730 ataatgatcatctgtttccaccaaagtacttaattttcttctcgttaaatcttg 789
DB 455 ataatgatcatctgtttccaccaaagtacttaattttcttctcgttaaatcttg 514
QY 790 cttgatcttcttttaacaaatccaaatgtagatacttctctcgttaaatc-aata 848
DB 515 cttgatcttcttttaacaaatccaaatgtagatacttctctcgttaaatc-aata 574
QY 849 acatgtaattc 859
DB 575 acatgtaattc 585
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RESULT 7

AAFS8252 standard; DNA: 936 BP.

ID AAF58252

AC AAF58252; 24-APR-2001 (first entry)

DE Oligonucleotide D1835.

KM Electron-transfer group; ETM; mismatch; genotyping;

KM gene expression; ss.

OS Synthetic.

PN WO200107665-A2.

PD 01-FEB-2001.

PE 26-JUL-2000; 2000MO-US20476.

PR 26-JUL-1999; 99US-0145695.

PR 17-MAR-2000; 2000US-0190259.

PA (CLIN-) CLINICAL MICRO SENSORS INC.

PI Umek RM;

DR WPI; 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface

PS Example 6; Page 127; 159pp; English.

CC The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.

SQ Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 12.5%; Score 116.8; DB 22; Length 936;
Best Local Similarity 6.3%; Pred. No. 1.1e-17;
Matches 55; Conservative 459; Mismatches 356; Indels 0; Gaps 0;

```
QY 63 ggaagtgacgtcgttagagatatagcgcggttaggaagaagaacgagatggttg 122
DB 905 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 846
QY 123 aagaagaatgaagtaacgaacgaacgagcgttgaaacgaagaagatgaggaatgat 182
DB 845 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 786
QY 183 tagtgaatcctgaagataattctgtctcgtgtgttaacagggcgaacatcgtggaatt 242
```

D	b	785	AA
Q	y	243	tggcgaagaattccagcaggacgctcgagacagtgttataatagtaagcgcgaatt
D	b	725	AA
Q	y	303	ctctccggttgaaagacgtgtcaatcacgaagaagaatcgtcggttcgttgtt
D	b	665	AA
Q	y	363	ctaacatcggaagaagaatcgaacgcggaagatcgattgttagactcgtggaataacg
D	b	605	AA
Q	y	423	gttcagcatgtgaaaacgaacgcgtcgtgatcttcgatgatgttaaatgaagtgaagaat
D	b	545	AA
Q	y	483	cgaatgacaatgattcttcttcgtgctgtttgaagatgtagaagtcgcgcgagtttaa
D	b	485	AA
Q	y	543	ggaagagtcctcattgagacggtgtaagaagctgaatgaagaatttttcaggctgcg
D	b	425	AA
Q	y	603	agaaagatcttcggaagaatgtgttggaatgttctatgaagtataactcgtattcgaga
D	b	365	AA
Q	y	663	aagatgagcacttggctggaggaagatacgaatggtgattaattgaatccatgaagaagac
D	b	305	AA
Q	y	723	gatgatgaatgatgatcatgttttcaccaaagtaactatatatttcttcctgtaata
D	b	245	AA
Q	y	783	atccttgcttgattttctttaacaaaaaccgaatgtagatacttcctcgataaa
D	b	185	AA
Q	y	843	tcaataacatgtaattcaacttggcttgtaacttctccttgagtgtaattaaatgatcgctg
D	b	125	AA
Q	y	903	ttttctcgattaaatacataatgattat
D	b	65	AA
RESULT 8 AAF58254/c ID AAF58254 standard; DNA; 936 BP. AC AAF58254; XX XX DT 24-APR-2001 (first entry) DE Oligonucleotide D1875. XX KW Electron-transfer group; ETM; mismatch; genotyping; RW gene expression; ss. XX OS Synthetic. XX XX MO200107665-A2. XX XX 01-FEB-2001. XX XX PD 26-JUL-2000; 2000MO-US20476. XX XX PF 26-JUL-1999; 99US-0145695. XX XX RR			

PR	17-MAR-2000; 2000US-0190259.
XX	
PA	(CLIN-) CLINICAL MICRO SENSORS INC.
XX	
PI	Umek RM;
XX	
DR	WPI; 2001-159728/16.
XX	
PT	Nucleic acids containing electron-transfer group, useful as labels in
PT	hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT	a single surface
XX	
PS	
XX	Example 6; Page 127; 159pp; English.
XX	
CC	The present invention relates to a composition comprising two nucleic
CC	acids each containing an electron-transfer group (ERM) having.
CC	different redox potentials. The invention is used for electronic
CC	detection of nucleic acids, especially of substitutions (mismatches)
CC	and single-nucleotide polymorphisms, e.g. for genotyping,
CC	monitoring gene expression.
XX	
SQ	Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

[illegible]


```
Qy 123 aagagaatgagttacgacgacggtgaaacgaagaatgaggaatgagatt 182
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 845 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 786

Qy 183 tagtgaatcaggataattctctccgtgtgtagcagcgacgaatcggtgaaattg 242
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 785 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 726

Qy 243 tggcgagaattcagcagcgctcgagacgaagtgtgtatcagtcagcgagatt 302
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 725 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 666

Qy 303 ctctccggttgaagaacagtgtaaatcgaaagaagatcgcttcgtgtgtt 362
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 665 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 606

Qy 363 ctacatcggaagagaatcgaaacggaatcgaaattgtagatcttgaggaataacg 422
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 605 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 546

Qy 423 gtgacgactgtaaacggaacgctcggtattcagatgatttgaataagaatgagaat 482
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 545 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 486

Qy 483 cgatgaacatgattctcttcgtgtgtgtgagatgtagtctcgccgaggttaa 542
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 426

Qy 543 ggaagagcttcacgagacggtgaaagaatgagtagaagatttttcaagtgcgcg 602
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 366

Qy 603 agaaagatctcggaataagttgttgaaatgctcagtaactcgaattcgaga 662
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 306

Qy 663 aagatgagccactggtggaagacagatcggttgaattgaatcagaaagaaac 722
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 305 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 246

Qy 723 gatgataatgataatgatttcaacaaagtaacttatttcttctgtaata 782
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 186

Qy 783 atcttctctgatttcttcttcaacaatcgaatgtagatcttctcctcgaataa 842
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 126

Qy 843 tcaataacatgtaactcaacttctgttactccttgaggttaataatgattcggtg 902
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 66

Qy 903 ttttctcagtaataaactataaatttat 932
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 36

RESULT 12
AAF58255/c
ID AAF58255 standard; DNA; 938 BP.
XX
XX AAF58255;
AC
XX 24-APR-2001 (first entry)
DE
XX Oligonucleotide D1876.
KW
XX Electron-transfer group; ETM; mismatch; genotyping;
XX gene expression, ss.
XX
XX Synthetic.
XX
XX WO200107665-A2.
PN
```

```
XX
XX 01-FEB-2001.
PD
XX
XX 26-JUL-2000; 2000WO-US20476.
PF
XX
XX 26-JUL-1999; 99US-0145695.
PR
XX 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
PA
XX
XX Dmek RM;
PI
XX
XX WPI; 2001-159728/16.
DR
XX
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
PS
XX
XX Example 6; Page 127; 159pp; English.
CC
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX
XX Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
SQ

Query Match 12.5%; Score 116.8; DB 22; Length 938;
Best Local Similarity 6.3%; Pred. No. 1.1e-17;
Matches 55; Conservative 459; Mismatches 356; Indels 0; Gaps 0;

Qy 63 ggaagtgactcgttagagattatgctgcggttagagaagaagaatgagattg 122
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 905 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 846

Qy 123 aagagaatgagttacgacgacggtgaaacgaagaatgaggaatgagattgatt 182
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 845 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 786

Qy 183 tagtgaatcaggataattctctccgtgtgtagcagcgacgaatcggtgaaattg 242
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 785 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 726

Qy 243 tggcgagaattcagcagcgctcgagacgaagtgtgtatcagtcagcgagatt 302
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 725 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 666

Qy 303 ctctccggttgaagaacagtgtaaatcgaaagaatcggttctcgtgtgtt 362
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 665 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 606

Qy 363 ctacatcggaagagaatcgaaacggaatcgaaattgtagatcttgaggaataacg 422
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 605 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 546

Qy 423 gtgacgactgtaaacggaacgctcggtattcagatgatttgaataagaatgagaat 482
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 545 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 486

Qy 483 cgatgaacatgattctcttcgtgtgtgtgagatgtagtctcgccgaggttaa 542
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 426

Qy 543 ggaagagcttcacgagacggtgaaagaatgagtagaagatttttcaagtgcgcg 602
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 366

Qy 603 agaaagatctcggaataagttgttgaaatgctcagtaactcgaattcgaga 662
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 306
```


XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

Query Match 11.9%; Score 111; DB 22; Length 936;
Best Local Similarity 1.0%; Pred. No. 2,4e-16;
Matches 6; Conservative 395; Mismatches 220; Indels 0; Gaps 0;

QY 312 ttgaagaacagtgccaatcgaagaagaattcggtcgttgcgttctacatcg 371
DB 132 www.
QY 372 aagagaatcgaacgaggaatcgaatttgatcttgaggaataacggtgacgac 431
DB 192 www.
QY 432 gtgaacagaacgctggtgattcgaatgattgaataagaagaggaatcgaatc 491
DB 252 www.
QY 492 tggattctctcgtggtcgttgaagatgtagatctcgcgcgacggttaaggaagtc 551
DB 312 www.
QY 552 tccatgagacggtgaagaagcgtgtagaagaatttttcaggtgcgagagaatgc 611
DB 372 www.
QY 612 ttcggaataagtgctggaatgctcgaatgaatcgaatcgaatcgaatgagc 671
DB 432 www.
QY 672 cactgtgtgaggaagacagagtggttaattgaatccctggaagaagacgatgc 731
DB 492 www.
QY 732 aatgatacatgtttcaccacaagtaactataattttctcgtataatcttgct 791
DB 552 www.
QY 792 ttgatttcttcaacaataccaatgtagatacttctcgcgaataacaataca 851
DB 612 www.
QY 852 tgaatacactttgttgcactcctcgtggaataataatagatcgttttctccg 911
DB 672 www.
QY 912 ataataaactaagttat 932
DB 732 www.

RESULT 15
AAF58257
ID AAF58257 standard; DNA; 936 BP.
XX
AC AAF58257;
XX
DT 24-APR-2001 (first entry)

XX Oligonucleotide D1954.
DE
XX Electron-transfer group; ETM; mismatch; genotyping;
XX
XX gene expression; ss.
XX
XX Synthetic.
XX
XX WO200107665-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US20476.
XX
XX 26-JUL-1999; 99US-0145695.
XX
XX 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX Unex RM;
XX
XX WPI; 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

Query Match 11.9%; Score 111; DB 22; Length 936;
Best Local Similarity 1.0%; Pred. No. 2,4e-16;
Matches 6; Conservative 395; Mismatches 220; Indels 0; Gaps 0;

QY 312 ttgaagaacagtgccaatcgaagaagaattcggtcgttgcgttctacatcg 371
DB 132 www.
QY 372 aagagaatcgaacgaggaatcgaatttgatagatctgaggaataacggtgacgac 431
DB 192 www.
QY 432 gtgaacagaacgctggtgattcgaatgattgaataagaagtagaatacgaatc 491
DB 252 www.
QY 492 tggattctctcgtggtcgttgaagatgtagatctcgcgcgacggttaaggaagtc 551
DB 312 www.
QY 552 tccatgagacggtgaagaagcgtgtagaagaatttttcaggtgcgagagaatgc 611
DB 372 www.
QY 612 ttcggaataagtgctggaatgctcgaatgaatcgaatcgaatcgaatgagc 671
DB 432 www.
QY 672 cactgtgtgaggaagacagagtggttaattgaatccatcgaagaagacgatgc 731
DB 492 www.
QY 732 aatgatacatgtttcaccacaagtaactataattttctcgtataatcttgct 791
DB 552 www.

[illegible]

Search completed: January 30, 2002, 11:56:16
Job time: 2855 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2002, 11:04:46 ; Search time 1206.98 Seconds
(without alignments)
8297.624 Million cell updates/sec

Title: US-09-574-735C-1
Perfect score: 932
Sequence: 1 ggcacggagggaaccacaaa.....ttaataacataagtttat 932

Scoring table: IDENTITY-NUC
Gap 10.0 , Gapext 1.0

Searched: 11351937 seqs, 537289281 residues
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estopl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hlc:*
10: gb_estl:*
11: gb_estl2:*
12: gb_hlc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	69.6	7.5	1101	13	CNS0039G
c 2	58.4	6.3	928	13	CNS00DKY
c 3	57.2	6.1	1101	13	CNS00EVL
c 4	56	6.0	997	13	CNS005TE
c 5	55.6	6.0	1092	13	CNS020K7
c 6	54.6	5.9	1101	13	CNS0039G
c 7	54	5.8	702	11	BF863173
c 8	53.8	5.8	1101	13	CNS000T2
c 9	53.4	5.7	1101	13	CNS017V2
c 10	52.8	5.7	1101	13	CNS00293
c 11	52.6	5.6	1225	13	CNS0161D
c 12	52	5.6	1101	13	CNS017KX

c 13	51.8	5.6	1201	13	CNS0163J	AL106249 Drosophila
c 14	51.4	5.5	1101	13	CNS00LJT	AL068307 Drosophila
c 15	51.2	5.5	970	13	CNS0182E	AL108800 Drosophila
c 16	50.6	5.4	1101	13	CNS00LJM	AL068473 Drosophila
c 17	50.4	5.4	467	13	CNS018G8	AL109298 Drosophila
c 18	50.4	5.4	996	13	CNS00DFH	AL071063 Drosophila
c 19	50	5.4	524	13	CNS01090	AL167541 Tetradon
c 20	49.8	5.3	1101	13	CNS00EJ4	AL069257 Drosophila
c 21	49.6	5.3	889	13	CNS006MT	AL065765 Drosophila
c 22	49.6	5.3	1083	13	CNS001H6	AL074775 Drosophila
c 23	49.4	5.3	1086	13	CNS000YK	AL096592 Drosophila
c 24	49.4	5.3	1101	13	CNS001FB	AL060732 Drosophila
c 25	49.2	5.3	1094	13	CNS012FZ	AL101513 Drosophila
c 26	49.2	5.3	1101	13	CNS000D1	AL065414 Drosophila
c 27	49	5.3	1002	13	CNS001XA	AL075355 Drosophila
c 28	48.8	5.2	697	13	A2124243	A2124243 T223107b
c 29	48.8	5.2	707	13	A2124244	A2124244 T223108b
c 30	48.8	5.2	1101	13	CNS00DFU	AL071076 Drosophila
c 31	48.8	5.2	3939	13	BH001059	BH001059 T122513b
c 32	48.6	5.2	1101	13	CNS016LI	AL106896 Drosophila
c 33	48.6	5.2	1101	13	CNS017KE	AL108152 Drosophila
c 34	48.4	5.2	876	13	CNS000G1	AL053529 Drosophila
c 35	48.4	5.2	887	13	A2544590	A2544590 ENTDE54TR
c 36	48.4	5.2	1063	13	CNS07A2Y	AL436064 T3 end of
c 37	48.2	5.2	607	13	BH004535	BH004535 BMBA608B2
c 38	48.2	5.2	906	13	A2527585	A2527585 ENTCE20TR
c 39	48.2	5.2	908	13	BH131383	BH131383 ENTND36TF
c 40	48.2	5.2	987	13	CNS00418	AL066537 Drosophila
c 41	48.2	5.2	1092	13	CNS020K7	AL175666 Tetradon
c 42	48.2	5.2	1101	13	CNS0026Z	AL097301 Drosophila
c 43	48	5.2	848	13	A2689328	A2689328 ENTHF58TF
c 44	48	5.2	905	13	CNS000KH	AL077798 Drosophila
c 45	48	5.2	1001	13	CNS0155H	AL105023 Drosophila

ALIGNMENTS

RESULT 1
CNS0039G/c
LOCUS
DEFINITION
CNS0039G 1101 bp DNA
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPC1-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL063921
AL063921.1 GI:4941778

fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosser in Pletier de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPC1-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	Location/Qualifiers
1. .1101	
source	/organism="Drosophila melanogaster"
	/db.xref="taxon.7227"
	/clone.lib="RC1-98"
	/clone="BAC08K10"
	/note="end : TET3"
BASE COUNT	201 a 64 c 131 g 202 t 503 others
ORIGIN	
Query Match	7.5% Score 69.6; DB 13; Length 1101;
Best Local Similarity	18.0%, Freq. No. 0.00079;
Matches 108; Conservative 245; Mismatch 247; Indels 0; Gaps 0;	
Y 310	ggttgaagaacagtgctcaatcagaagaagattcgtcggttcgtgtgttcacatc 369
Db 997	RGAGCRDDAATDADGAGRRDGRKRRKKDDDDDKGGKKKAAKAAWATKRWMD 938
Y 370	ggaagaagaatcgaacggaagaatctgttagatctcttggaanaataacggtga 429
Db 937	WDMKDKMKWDGAKDKRRADDGAGCKDDGKKADDDDDTGCTKDDDKKMKDWKAKCT 878
Y 430	tcgtgaacagagaacgtcgtgattacgatatttgaataagagtggaatcgatga 489
Db 877	WGDATWAMATWTWWGWDADWMTDAAADWMAADRRDAAWAKMKDDAMGAKARDKR 818
Y 490	catgattctcttcgtgtcgcttggaagatgtagagtcgcgcgagttagaagaag 549
Db 817	DWGDRAGKRGKAGRRRRRADDKRDAAADRDAAATWTTTTHDITDWMKKTDTYWR 758
Y 550	tctcatgagacggtgaagaagctgagttgaagaatttttcaggtgcgagagaaga 609
Db 757	WADRTWDDDDDDRRACATAGRKWRKRRKRRKRDFTWDDADADTARDORRRGDG 698
Y 610	tcttcggaataagttcttggaatggtctcgaagtaataactcgattcgagaagaatga 669
Db 697	ADAGKCKTKGRRRRRRDRATWDTDAWMAADAAWMTTDTDTDDMKDRRRKCARRRRT 638
Y 670	gccacttggtgagaagaatacgaagtggtaaatgaatccatgagaagaacgatgatg 729
Db 637	TARAADWMTTWKAMPADWAKDKMTFADRWWRWMAADTWTDAKRDWAKARAWARDRAR 578
Y 730	ataatgatcatcattgtttccacaaagctattatatttctcttgtaataacttg 789
Db 577	AANADRRWTKGTTTATATWTTWAAARAAWMAWMAATTATATWTTTWTWTTT 518
Y 790	cttggtttttctttaaacaataccaaatgttagatactcttcgataatacaata 849
Db 517	WTTTAAWMAWMAWMTATWMAWMAAAMAAAAAATTTTTTTTTTAAWTAAMWTAWT 458
Y 850	catgaataccaactttgttgtaacttccttggaagtaataatgaatcgtgttttc 909
Db 457	WTTTWTWTTTMAATTTTTTTWTTWMAATTAATTTTTTWTWAAAAAAMWMTWTAT 398
RESULT 2	
CNS00DKY/C	928 bp DNA GSS 04-JUN-1999
LOCUS	Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION	BAC27424 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL071865
VERSION	AL071865.1 GI:4948170
KEYWORDS	GSS.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 928)
AUTHORS	Genoscope.
TITLE	Direct Submssion

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
Location/Organism

1. 928
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lid="RPCL-98"
/clone="BACR27A24"
/note="end : T7"

BASE COUNT 262 a 70 c 84 g 321 t 191 others

ORIGIN

Query Match 6.3%; Score 58.4; DB 13; Length 928;
Best Local Similarity 31.9%; Pred. No. 0.11; Gaps 0;
Matches 72; Conservative 67; Mismatches 87; Indels 0;

QY 701 aaatgacatccagagaagaagcagatgatataatcatgtttccaccsaagtac 760
||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 865 AAAAAMWTTTCMAAAAMAMMNCVMKMMAMMMMMMMMMMMMTTMMNNHNNHHNMTTTTT 806

QY 761 ttattatttcttccttgtaaatcttgtcttgtagtttctctttaacaatatcaatg 820
||| ||| ||| ||| :
Db 805 TTWTTT 746

QY 821 tagatatcttcctcgcgaataacataacatglaattcaacttgcttgtaacctt 880
::: ||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 745 WMMWWATATTATTGTATWTWAMATAMAAAAAAAAMWTAATTTTWTATTATTTGTA 686

QY 881 gaggcataatgaattcggtgttttctcgattaaactaata 926
||| : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 685 AAATTTTATTTATTTTATTTTATTTTATTTATATATATATATATA 640

RESULT 3
CNS00EVL/c 1101 bp DNA GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR29523 of RPCL-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL069706
ACCESSION AL069706.1 GI:4949849
VERSION
KEYWORDS
SOURCE GSS
ORGANISM fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)

TITLE - Web : www.genoscope.cns.fr
JOURNAL
COMMENT
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1lb="RPCI-98"
/clone="BACR29B23"
/note="end : T7"

BASE COUNT 419 a 91 c 60 g 299 t 232 others

ORIGIN

Query Match 6.1%; Score 57.2; DB 13; Length 1101;
Best Local Similarity 38.0%; Pred. No. 0.18;
Matches 89; Conservative 46; Mismatches 99; Indels 0; Gaps 0;

Qy 699 ttaaatgaaatcgaagaacgagatgataatgataatgattgtttcaccacaagt 758
Db 1003 TWTATMTAAATATATATAAATAATATAAATAAATAAATAAATAAATAA 944
Qy 759 acctatattttcttcgtaataatcttgccttgccttcttaccacaatccaa 818
Db 943 TATATMTAT 884
Qy 819 tctgataatcttctcgaataatcaataatgataatcaacttcttgcatacc 878
Db 883 TWTATMTAT 824
Qy 879 ttgaggaatcaatagatcgttcttctcgaataatcaataatgattat 932
Db 823 WTTATMTAT 770

RESULT 4

CNS005TE/c 997 bp DNA GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION A1060767
VERSION A1060767.1 GI:4943573
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 997)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org>. The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Oseogawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial

AUTHORS

JOURNAL

COMMENT

melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..997
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1lb="RPCI-98"
/clone="BACR12K22"
/note="end : TET3"

BASE COUNT 89 a 99 c 13 g 258 t 538 others

ORIGIN

Query Match 6.0%; Score 56; DB 13; Length 997;
Best Local Similarity 18.8%; Pred. No. 0.31; Mismatches 264; Indels 1; Gaps 1;
Matches 104; Conservative 185; Mismatches 264; Indels 1; Gaps 1;

Qy 78 agagattatgcygcygtagagagaagaaagagatggttgtaagaatggagta 137
Db 997 ARARRRAGARARARARRRRRRCGARGARARARRRRRARGARARARAGARAG 938
Qy 138 cgaagcagcagtgtaacgaagaagatgagaggaagtgtatttagtgatctaga 197
Db 937 AGARARARARRRRRRRRRRRGRAGRAGRSAGCGGRRRAAARADARARARAR 878
Qy 198 taattcttcctcggtgtacagcgcaatcgcgcgtggaattgtgacgaatcag 257
Db 877 ARRRARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 818
Qy 258 cagagcgcgcgaagacgagtggtttagtagtaacgagcgcgagatctcctcggtgaag 317
Db 817 ARARARRRRARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 758
Qy 318 aacggtgccaatcgaagaagaagatcgtcgttctgtgtctcaccgcgaagga 377
Db 757 RARARAGARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 698
Qy 378 aatcgaacgagaaatcga-atttgatcttggaagaataacggtgacatcgtga 436
Db 697 ARRR 638
Qy 437 aacgaacgctcgtgattacgattgataaagaatgaggaatcgaatcgaat 496
Db 637 RGARR 578
Qy 497 tcttctcgtggtcgtggaagatgtagatcgcgcgcggaatgaagaagatccat 556
Db 577 RRR 518
Qy 557 gagaagcgaagaagcgtgattgaagaatttttcaggtgagcgaagaatcctcg 616
Db 517 RRR 458
Qy 617 aataagttgctgga 630
Db 457 NNNNNNNNNNNNA 444

RESULT 5

CNS020K7/c 1092 bp DNA GSS 12-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 22L11 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION A1175696
VERSION A1175696.1 GI:7813753
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis

AUTHORS
Grossman, A., Davies, J., Federspiel, N., Harris, E., Hauser, C.,
Lefebvre, P., Modermont, J. P., Shrager, J., Silfow, C. and Stern, D.
TITLE
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 3
JOURNAL COMMENT
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27706-1000
Tel.: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES
source location/Qualifiers
1..702
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress condition I,
normalized, lambda zap II"
/note="Vector: pbluescript II SK-, Site.1: EcoRI, Site.2:
XhoI; This library, constructed by John Davies and Jeffrey
McMormot, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min,
1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, 1hr
, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda zap II
(Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT
ORIGIN
193 a 103 c 136 g 270 t

Query Match
Best Local Similarity 57.4%; Score 54; DB 11; Length 702;
Matches 117; Conservative 0; Mismatches 85; Indels 2; Gaps 1;

OY 721 taatgatgcatcgttttcaccaaagtcaactaatcttctctcgtaataatctgcg 790
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 463 TAATTAATAATATTATTTTAAATTAATTTGGTTATTTTATTTTATTTTAA 522
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 791 ttgatcttctttaacaaatccaagttagatat--cttctctcgaaataacaata 848
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 523 TTTCATTTTTTGTTTAAATTTTATATATATTTATTTATTTAAATTTTAA 582
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 849 acatgttaactcttgcttgtaacctcccttgaggtaattaattagatcggttttc 908
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 583 ATAACTAATATCATATTTTATATATATTAATAAGACATTAATTCAGTTATTTTGTG 642
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 909 tcgattataaactaactaagtttat 932
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 643 ACTATATTTTACTATTAAGATTAAT 666
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT
8
CONSOLUT2
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
ORGANISM
SOURCE
REFERENCE

CNS001T2 1101 bp DNA GSS 14-JUN-1999
Drosophila melanogaster genome survey sequence TERT3 end of BAC:
BACR48P19 of Rpci-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL078714
AI078714.1 GI:5102004
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

AUTHORS	Genoscope.									
TITLE	Direct Submission									
JOURNAL	Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr - Web : www.genoscope.cns.fr)									
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuoto Oseguwa and Aaron Mammosses in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .									
FEATURES	Location/Qualifiers									
Source	1..1101									
	/organism="Drosophila melanogaster"									
	/db_xref="taxon:7227"									
	/clone_lib="RPCI-98"									
	/clone="BACR48P19"									
	/note="end : TER3"									
BASE COUNT	469 a 6 c 69 g 151 t 406 others									
ORIGIN										
Query Match	5.8% ; Score 53.8; DB 13; Length 1101;									
Best Local Similarity	38.5% ; Pred. No. 0.81; Mismatches 100; Indels 0; Gaps 0;									
Matches	89; Conservative 42; Mismatches 100; Indels 0; Gaps 0;									
Qy	701 aaatgaatccatggaagaacgacgatgataatgatgatacattgttccacaaagtac 760									
Db	463 AAAAAAAAAAAAAAAAAAAATTTTGTTTTWWKATTTTWTDDADDKMAAMWD 522									
Qy	761 ttataattttcttcgtaataactcttgcttgatttcttctaacaatccaagt 820									
Db	523 TTTTAAWTTTWTAAATATATTTTWTWKATKTDTWKAKATAATMAAMWTTT 582									
Qy	821 tagatactttcttcgcgaataatcaataacatgataatcaactttgttgaacttc 880									
Db	583 TTTTAAWTTTWTWTAKKTWAMKAMWAFATTTTWTWTWTWMAATTTTWT 642									
Qy	881 gaggaataatagatcgcttttcttcgcgtaataaactaagaattta 931									
Db	643 TWTAAATTTTTTTTTTAKTKTTTTTTTTTTTATTAATAAATAAAWTTTDWA 693									
RESULT	9									
LOCUS	CNS017V2									
DEFINITION	Drosophila melanogaster genome survey sequence Sp6 end of BAC BACN37L10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.									
ACCESSION	AL108536									
VERSION	AL108536.1 GI:5628840									
KEYWORDS	GSS.									
SOURCE	fruit fly.									
ORGANISM	Plasmid Drosophila melanogaster									
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.									
REFERENCE	1 (bases 1 to 1101)									
AUTHORS	Genoscope.									
TITLE	Direct Submission									
JOURNAL	Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr - Web : www.genoscope.cns.fr)									
COMMENT	Determination of this BAC-end sequence was carried out as part of a									

COMMENT Determination of this BAC-end sequence was carried out as part of a

```
/organism="Drosophila melanogaster"  
/plasmid="pBelobAC1"  
/db_xref="taxon:7227"
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Best Local Similarity 39.6%; Pred. No. 1.9;
Matches 101; Conservative 35; Mismatches 119; Indels 0; Gaps 0;

Qy	677	ggttgagaagaagtaacgaatgggttaattcaatccatgaaagaacgatgcataa	736
Db	965	GGGRRGGGMMNNNNGGGGGGGGAAGGGCKTAAANAAAAATTTMAATWTTWWTW	906
Qy	737	tgaactcgtttccacaagbaactattaatttccttcgtataactcgttggat	796
Db	905	MAWMWMTTKAATTATTTTTWTMNAANAATAKKTWAWTMNAAMWMTAKTATTTWMT	846
Qy	797	tttcttttaaaaaaatccaatgtagatccttcctccgaataatcataacatgtaa	856
Db	845	TWTTTTTRAKRRAAAATATTTARAAAARKTKTAATTTAAGATTAAATTTATGTAA	786
Qy	857	ttcaacttttgttgcbaactccctgaagtaataatagatcgltttlcccgattaa	916
Db	785	ATTCAGATGTTATGAGATAATAATTAATTTATAGTTAATAAKTATTAATTTAMAATTTA	726
Qy	917	taaacataagtta 931	
Db	725	AAAAATRTAAATTTA 711	

RESULT 14	CNS00LJT/c	LOCUS	DEFINITION
	CNS00LJT	1101 bp	DNA
			GSS
			03-JUN-1999
			T7 end of BAC:
			BACR01P10 of RPCT-98 library from <i>Drosophila melanogaster</i> (fruit fly), genomic survey sequence.

BASE COUNT	507 a	148 c	112 g	171 t	163 others
ORIGIN					

Query Match	5.5%	Score 51.4;	DB 13;	Length 1101;
Best Local Similarity	45.7%;	Pred. No. 2.3;		
Matches 79;	Conservative 24;	Mismatches 70;	Indels 0;	Gaps 0.

```

Oy  742 atgctttccaccaagactatattttcttcgtaatactcttgatgttttc 801
      ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  359 wttttttttttttttttttttttttttttttttttttttttttttttttttttt
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy  802 tttaacaaatccaatgtagatctctctcgcgaataccaataatgtaattcaa 861
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  299 tttttcmaagtttttktttgatatttttttttttttttttttttttttttt
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy  862 ctttgcttgactccttgaglaattaatagatcgtttttctcgatt 914
      ||| ||| : : : ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  239 ttttgcttttttttttttttttttttttttttttttttttttttttttttttt
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT	15
CNS0182E	
LOCUS	
DEFINITION	
	CNS0182E 970 bp DNA GSS 26-JUL-1999
	Drosophila melanogaster genome survey sequence T7 end of BAC
	BACN37A19 of DrosBAC library from Drosophila melanogaster (fruit
	fly), genomic survey sequence.

BASE COUNT	214 a	147 c	153 g	315 t	141 others
ORIGIN					

Query Match	5.5%;	Score 51.2;	DB 13;	Length 970;
Best Local Similarity	35.6%;	Pred. No. 2.6;		
Matches	72;	Conservative 48;	Mismatches 82;	Indels 0;
				Gaps 0;

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2002, 11:07:41 ; Search time 45.26 seconds
(without alignments)
4663.665 Million cell updates/sec

Title: US-09-574-735C-1

Sequence: 1 ggcacggaggaaccacaa.....ttaataactaatttat 932

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/prodata/2/lna/6B_COMB.seq:*
5: /cgn2_6/prodata/2/lna/PCUTUS_COMB.seq:*
6: /cgn2_6/prodata/2/lna/backfilesl.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	76.2	8.2	7218	1 US-08-232-463-14	Sequence 14, App1
C 2	49	5.3	51952	3 US-08-947-823-1	Sequence 1, App1
C 3	44.4	4.8	19124	2 US-08-487-826-13	Sequence 13, App1
C 4	44	4.7	1689	1 US-07-991-867B-41	Sequence 41, App1
C 5	44	4.7	1689	2 US-08-544-332-41	Sequence 41, App1
C 6	44	4.7	8457	1 US-07-991-867B-1	Sequence 1, App1
C 7	44	4.7	8457	2 US-08-544-332-1	Sequence 1, App1
C 8	41.8	4.5	471	4 US-09-385-982-58	Sequence 58, App1
C 9	41.6	4.5	4090	4 US-08-569-214-4	Sequence 4, App1
C 10	40.2	4.3	837	4 US-08-937-236-4	Sequence 4, App1
C 11	40.2	4.3	837	4 US-08-998-416-288	Sequence 288, App1
C 12	38.6	4.1	6243	2 US-09-056-075-1	Sequence 1, App1
C 13	38.2	4.1	1113	1 US-08-231-342-5	Sequence 5, App1
C 14	37.8	4.1	12124	1 US-08-181-271A-36	Sequence 36, App1
C 15	37.8	4.1	12124	1 US-08-449-315-36	Sequence 36, App1
C 16	37.8	4.1	12124	1 US-08-449-315-36	Sequence 36, App1
C 17	37.8	4.1	12124	1 US-08-449-315-36	Sequence 36, App1
C 18	37.8	4.1	12124	1 US-08-456-265A-36	Sequence 36, App1
C 19	37.8	4.1	12124	1 US-08-455-416-36	Sequence 36, App1
C 20	37.8	4.1	12124	1 US-08-455-244-36	Sequence 36, App1
C 21	37.8	4.1	12124	1 US-08-454-876-36	Sequence 36, App1
C 22	37.8	4.1	12124	2 US-08-457-364-36	Sequence 36, App1
C 23	37.8	4.1	12124	2 US-08-456-262-36	Sequence 36, App1
C 24	37.8	4.1	12124	2 US-08-456-240-36	Sequence 36, App1
C 25	37.8	4.1	12124	2 US-08-455-736-36	Sequence 36, App1
C 26	37.8	4.1	12124	2 US-08-971-217-36	Sequence 36, App1
C 27	37.8	4.1	12124	4 US-09-350-600-36	Sequence 36, App1

28	37.6	4.0	615	4 US-08-998-416-186	Sequence 186, App
C 29	37.4	4.0	2781	3 US-08-749-522-4	Sequence 4, App1
C 30	37.2	4.0	5852	1 US-07-867-106-2	Sequence 2, App1
C 31	37	4.0	1680	4 US-08-943-731-166	Sequence 166, App
C 32	37	4.0	17606	4 US-08-943-731-4	Sequence 4, App1
C 33	36.8	3.9	636	4 US-08-998-416-1137	Sequence 1137, App
C 34	36.4	3.9	19124	2 US-08-487-826B-13	Sequence 13, App1
C 35	36.2	3.9	734	3 US-09-014-583-1	Sequence 1, App1
C 36	36.2	3.9	1667	1 US-08-485-284A-1	Sequence 1, App1
C 37	36.2	3.9	6768	1 US-08-107-755A-1	Sequence 1, App1
C 38	36.2	3.9	8457	1 US-07-991-867B-1	Sequence 1, App1
C 39	36.2	3.9	8457	2 US-08-544-332-1	Sequence 1, App1
C 40	36	3.9	6216	3 US-09-213-053-1	Sequence 1, App1
C 41	36	3.9	8920	2 US-08-446-855A-1	Sequence 1, App1
C 42	36	3.9	8920	4 US-09-150-741-1	Sequence 1, App1
C 43	35.8	3.8	319	1 US-07-593-657-14	Sequence 14, App1
C 44	35.8	3.8	3095	6 US-08-998-416-487	Sequence 487, App
C 45	35.6	3.8	872	4 US-08-998-416-487	Sequence 487, App

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935, 313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-Fls
US-08-232-463-14

REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13

Query Match 4.88; Score 44.4; DB 2; Length 19124;
Best Local Similarity 52.7%; Pred. No. 0.055;
Matches 96; Conservative 0; Mismatches 86; Indels 0; Caps 0;

QY 725 tgaagataagatgatactggtttccacaaagtaactatttcttctgtaataat 784

Db 15649 TTAATTTTAAATGATGATTTTAAATTAATAAATTTTAAATTTTAAATTTTGAATA 15590

QY 785 ctctgcttgatcttctttaaacaatccaaatgagatcttctcgcgaataac 844

Db 15589 ATCTTTTCAATTTTATTTCTATCAAAATTTATATTTATATATTTTATTTT 15530

QY 845 aataacatgaatcaacttctgttctactccttgagtaataatagatcgtgt 904

Db 15529 AAAAAATTTTCTCTTTTATTTTATTTTATTTTAAATAAATTTTATTAAT 15470

QY 905 tt 906

Db 15469 TT 15468

RESULT 4

US-07-991-867B-41
Sequence 41, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781e1 Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991

ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP114.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-991-867B-41

Query Match 4.78; Score 44; DB 1; Length 1689;
Best Local Similarity 52.1%; Pred. No. 0.033;
Matches 98; Conservative 0; Mismatches 90; Indels 0; Caps 0;

QY 743 ttgtttcaccagaagtactatttcttctcgtataatcttctgttatttct 802

Db 667 TTTTTCATATTCATCATATATATATATATATATATATATATATATATATATCT 726

QY 803 tttaacaatccaaatgagatgatacttctcgcgaataacataatgtaattcaac 862

Db 727 TTTTAAACATATATAGCTATATATATATATATATATATATATATATATATATCT 786

QY 863 ttctgttctactccttgagtaataatagatcgtgttctcgcgaataaact 922

Db 787 ATATATATATATATCTCTTTATATATATATATATATATATATATATATATATAT 846

QY 923 ataagtt 930

Db 847 ATTAAT 854

RESULT 5

US-08-544-332-41
Sequence 41, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777e1 Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE: 07-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992

Query Match	4.7%;	Score 44;	DB 2;	Length 1689;
Best Local Similarity	52.1%;	Pred. No. 0.033;		
Matches 98;	Conservative 0;	Mismatches 90;	Indels 0;	Gaps 0;

```

RESULT 6
US-07-991-867B-1
; Sequence 1, Application US/07991867B
; Patent No. 5476781
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
; TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/991,867B
; FILING DATE: 12-DEC-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/14818
; FILING DATE: 12-FEB-1992

```

```

Query Match          4.7%; Score 44; DB 1; Length 8457;
Best Local Similarity 52.1%; Pred. No. 0.054;
Matches 98; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 743 ttgtttccaccaagaactactatattttctctgttaataactctgttgattttct 802
      || |||| | | | | | | | | | | | | | | | | | | | | | |
Db 7435 TTTTTCATGATTCATGCTATATATATTTGTTCTGTTAACATGCTTCATTTAATCT 7494

QY 803 tttaacaaatccaaatgtatagatctctctcgcgaataatcaataacatgtaaltcaac 862
      ||| | | | | | | | | | | | | | | | | | | | | | | |
Db 7495 TTTTATGAGAAATATAGCTAATTAATGTTTCTCTTAATTCCTTAAATTAATTAACCTTCC 7554

QY 863 ttgtgttgactacctgtgaagttaattaatagattcggtttttctcgatataaacact 922
      ||| ||| | | | | | | | | | | | | | | | | | | | |
Db 7555 ATTATTTATATATATTCCTCTTTATATTCATCAACATTGGCTTAAGTAACCATTTAAATT 7614

QY 923 ataagtt 930
      || | | |
Db 7615 ATTAAATT 7622

RESULT 7
US-08-544-332-1
; Sequence 1, Application US/08544332
; Patent No. 5935777
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System

```


NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Gerard H. Bencen
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/544,332
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/991,867
 FILING DATE: 07-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/107,755
 FILING DATE: 19-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 92/14818
 FILING DATE: 12-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,685
 FILING DATE: 30-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/657,584
 FILING DATE: 19-FEB-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Bencen, Gerard H.
 REGISTRATION NUMBER: 35,746
 REFERENCE/DOCKET NUMBER: UFI14.C4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8457 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Amsacta moorei entomopoxvirus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: complement (65..1459)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1474..2151
 FEATURE:
 NAME/KEY: CDS
 LOCATION: complement (2239..2475)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 2502..2987
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3080..6091
 FEATURE:
 NAME/KEY: CDS
 LOCATION: complement (6277..6768)
 US-08-544-332-1

Query Match 4.7%; Score 44; DB 2; Length 8457;
 Best Local Similarity 52.1%; Pred. No. 0.054;
 Matches 98; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 743 tgcgttaccacaagtaactatatttctctgtaataatccttgcttgatttctt 802
 || |||| | || |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 7435 TTTTTCATATCCATCATATATATATATATATATATATATATATATATAT 7494
 Qy 803 tttaacaataatcgaatgtagatatttctctcgataatcaatgaatcaac 862
 |||| | || | || |||| || || || || || || || || || || || || ||
 Db 7495 TTTATAAGAACATATACCTATATATATATATATATATATATATATATAT 7554
 Qy 863 ttgttgtaactccttgaggaatgaatgaatgaatgaatgaatgaatgaat 922
 || || || || || || || || || || || || || || || || || || || || ||
 Db 7555 ATTATTTAT 7614
 Qy 923 ataagtt 930
 || || || || || || || || || || || || || || || || || || || || ||
 Db 7615 ATTAAATT 7622
 RESULT 8
 US-09-385-982-58
 ; Sequence 58, Application US/09385982
 ; Patent No. 6262334
 ; GENERAL INFORMATION:
 ; APPLICANT: ENDEGE, WILSON O., ET AL.
 ; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
 ; TITLE OF INVENTION: PRODUCTS: II
 ; FILE REFERENCE: CCDA-260XX
 ; CURRENT APPLICATION NUMBER: US/09/385,982
 ; CURRENT FILING DATE: 1999-08-30
 ; EARLIER APPLICATION NUMBER: 09/328,111
 ; EARLIER FILING DATE: 1999-06-08
 ; EARLIER APPLICATION NUMBER: 60/117,393
 ; EARLIER FILING DATE: 1999-01-27
 ; EARLIER APPLICATION NUMBER: 60/098,639
 ; EARLIER FILING DATE: 1998-08-31
 ; NUMBER OF SEQ ID NOS: 344
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 58
 ; LENGTH: 471
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(471)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-385-982-58

Query Match 4.5%; Score 41.8; DB 4; Length 471;
 Best Local Similarity 54.1%; Pred. No. 0.077;
 Matches 85; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
 Qy 759 actataatttctctgtaataatccttgcttgatttcttcttaacaatacca 818
 || || || || || || || || || || || || || || || || || || || || ||
 Db 80 attgattatttatttctgtaataatccttcttcatagatttcttaaaagatt 139
 Qy 819 tgtagatatttctctcgataatcaatgaatgaatgaatgaatgaatgaat 878
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 Db 140 atcatgcacttggtcagaataataataataataataataatgatttgatcc 199
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 US-08-569-214-4/C
 ; Sequence 4, Application US/08569214
 ; Patent No. 6165469
 ; GENERAL INFORMATION:
 ; APPLICANT: MANN, BARBARA J.
 ; APPLICANT: PETRI, WILLIAM A.
 ; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
 ; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE


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Query Match          4.1%; Score 38.6; DB 2; Length 6243;
Best Local Similarity 48.0%; Pred. No. 1.1;
Matches 110; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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US-08-231-342-5/c
Sequence 5, Application US/08231342
Patent No. 5827684

GENERAL INFORMATION:
APPLICANT: Sreekrishna, Kotilanyadanam
APPLICANT: Prevatt, William D
APPLICANT: Thill, Gregory P
APPLICANT: Davis, Geneva R
APPLICANT: Koutz, Patricia
APPLICANT: Barr, Kathryn A
APPLICANT: Hopkins, Sharon A
TITLE OF INVENTION: Production of Bacillus Entomotoxins in Methylothrophic Yeast

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FILING DATE: 18-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: TC 07 0037 107

Oy 761 ttattatttctcgtcataatccttgcttcgtaatttctttaacaaat 813
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Db 5690 TTAATAATATGTTAAATATTAAGTATATCTCTAATATTTTTTTAAAAAAAT 5636

Thu Jan 31 09:50:44 2002

us-09-574-735C-1.rn1

Page 10

Search completed: January 30, 2002, 11:54:29
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ACCESSION A98054
VERSION A98054.1 GI:6781292
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS De,A.J. and De,V.L.
TITLE CYCLIN-DEPENDENT KINASE INHIBITORS AND USES THEREOF
JOURNAL Patent: WO 9914331-A 1 25-MAR-1999;
ALMEIDA JANICE DE (BE); LANDRIEU ISABELLE (BE)
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
ALMEIDA JANICE DE (BE); LANDRIEU ISABELLE (BE)
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DEFINITION Sequence 6 from Patent WO964599.
ACCESSION AX008796
VERSION AX008796.1 GI:9996260
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 755)
Fowke, L.C., Wang, H. and Crosby, W.L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 9964599-A 6 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRI-FOOD CANAD (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV SASKATCHEWAN TECHNOLOGIES (CA)

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DEFINITION Arabidopsis thaliana cyclin-dependent kinase inhibitor protein (ICK1) mRNA, complete cds.
ACCESSION U94772
VERSION U94772.1 GI:2052501
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
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AUTHORS
TITLE
JOURNAL
Mang, H., Fowke, L.C. and Crosby, W.L.
A plant cyclin-dependent kinase inhibitor gene
Nature 386 (6624), 451-452 (1997)
2 (bases 1 to 856)
Mang, H., Fowke, L.C. and Crosby, W.L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 9964599-A 6 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRI-FOOD CANAD (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV SASKATCHEWAN TECHNOLOGIES (CA)

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 ACCESSION AX008791
 VERSION AX008791.1 GI:9996255
 KEYWORDS

SOURCE
 ORGANISM
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 904)
 FOLKE, L.C., WANG, H. and CROSBY, W.L.
 Cytlin dependent kinase inhibitors as plant growth regulators
 Patent: WO 964599-A 16-DEC-1999; AGRICULTURE AND AGRIFOOD CANAD
 FOLKE LARRY C (CA); WANG HONG (CA); CROSBY WILLIAM L (CA); UNIV
 (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
 SASKATCHEWAN TECHNOLOGIES (CA)

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 Percent Similarity: 55.897 Percent Identity: 34.359

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seq_documentation_block: 927 bp mRNA PLN 11-JAN-2001
 LOCUS AB029483
 DEFINITION Pisum sativum cki mRNA for cyclin dependent kinase inhibitor,
 complete cds.
 ACCESSION AB029483
 VERSION AB029483.1 GI:12081914
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Fabales; Fabaceae; Papilionoideae; Viciae;
 Pisum.

REFERENCE
 1 (bases 1 to 927)
 Shimizu-Sato,S. and Mori,H.
 A cDNA from Pisum sativum encoding the cyclin-dependent kinase
 inhibitor (CKI) homologue
 JOURNAL
 2 (bases 1 to 927)
 Shimizu-Sato,S. and Mori,H.
 Published only in Database (2001) In press

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seq_name: gb_pat:AX008793

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LOCUS AX008793 660 bp DNA PAT 06-SEP-2000
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ACCESSION AX008793
VERSION AX008793.1 GI:9996257
KEYWORDS
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ORANISM thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 660)
Fowke, L.C., Wang, H. and Crosby, W.L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 964599-A 3 16-DEC-1999;
FOUKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 642)
AUTHORS Fowke, L.C., Wang, H. and Crosby, W.L.
TITLE Cyclin-dependent kinase inhibitors as plant growth regulators
JOURNAL Patent: WO 9964599-A 8 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRI-FOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
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seq_documentation_block: 591 bp mRNA 26-JUL-2001
LOCUS ATH301557
DEFINITION Arabidopsis thaliana mRNA for cyclin-dependent kinase inhibitor 6
(krip6 gene).
ACCESSION AJ301557
VERSION AJ301557.1 GI:14422294
KEYWORDS cyclin-dependent kinase inhibitor; krip6 gene.
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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 591)
De Veylder, L., Beeckman, T., Beemster, G.T., Kriols, L., Terras, F.,
Landrieu, I., Van Der Schueren, E., Maes, S., Naudts, W. and Inze, D.
Functional Analysis of Cyclin-Dependent Kinase Inhibitors of
Arabidopsis
The Plant Cell. 13 (7), 1653-1668 (2001)
PUBMED 11449057
REFERENCE
2 (bases 1 to 591)
de Veylder, L.
Direct Submission
Submitted (31-OCT-2000) De Veylder L., Departement Plantegenetica,
Vlaams Interuniversitair Instituut voor Biologie (VIB), K.L.
Ledeganckstraat 35, B-9000 Gent, BELGIUM
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1. 591
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ACCESSION AX008797
VERSION AX008797.1 GI:9996261
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Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 824)
REFERENCE
AUTHORS Fowke,L.C., Wang,H. and Crosby,W.L.
TITLE Cyclin-dependent kinase inhibitors as plant growth regulators
JOURNAL Patent: WO 9964599-A 7 16-DEC-1999.
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRI-FOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
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seq_name: gb_pat:AX008805

seq_documentation_block:
LOCUS AX008805 804 bp DNA PAT 06-SEP-2000
DEFINITION Sequence 15 from Patent WO9964599.
ACCESSION AX008805
VERSION AX008805.1 GI:9996264
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. red goosefoot.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
1 (bases 1 to 804)

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PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139470.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 19-JUL-1999; 99US-0144325.
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PR 20-JUL-1999; 99US-0144335.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.

PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
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158 TACAGCAGCGCGGTGAACGAGAGATGAGAGAGATGATTTAG 207
34 aLgIuSerArgLleIleLeuSerProCysValGlnAlaThrAsnArgGly 50
208 TGGAAATCTAGATTAATCTCTGCTCGTACAGCGCACAAATCGCGT 257
51 GlyTLeValAlaArgAsnSerAlaGlyAlaSerLeuThrSerValVal 67
258 GGAATTTGGGAGAAATTCAGCAGAGCGTCGAGAGAGATGTTGTTAT 307
67 eValArgArgArgAspSerProProValGluGluGlnCysGlnIleGlu 84
308 AGTACGACGGGAGATTCCTCCGCGTTGAAGAACAGTCAATCGAAG 357
84 LgluIAspSerSerValSerCysSerThrSerGluGluLysSerLys 100
358 AAGAAGATTCTCGCTTCGTTCTTACATCGAAGAGAAATCGAAA 407
101 ArgArgIleGluPheValAspLeuGluGluAsnGlnLysAspArgGly 117
408 CGGAGAAATTCGATTTGATCTTGAGAGAAATACCGTGCATTCGTGA 457
117 uThrGluThrSerTrpIleArgAspAspLeuAsnLysSerGluLys 134
458 AACAGAAACGTCGTGATTTACATGATTTGAATAGAGTGAAGATCGA 507
134 eTAsnMetAspSerSerSerValAlaValGluAspValGluSerArgArg 150
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151 ArgLeuArgLysSerLeuHisGluThrValLysGluValGluLeuGluAs 167
558 AGGTTAAAGAGAGATCTCCATGACAGCGTGAAGAGCTGATTAGAGA 607
167 PphePheGlnValAlaGluLysAspLeuArgAsnLysLeuLeuGlyCys 184
608 CTTTTCAGGTGGCGGAGAAAGATCTCGAATAGTGTGGAGTGT 657
184 eMetLysTyrAsnPheAspPheGluLysAspGluProLeuGlyGly 200
658 CTATGAAGTATTAATCTGATTTGAGAAAGATGAGCCACTGTGGAGGA 707
201 ArgTyrGluTrpValLysLeuAsnPro 209
708 AGATACGAGTGGTTAAATTCGAATCCA 734
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ID AAC37798 standard; DNA; 886 BP.
AC AAC37798;
XX
DT 17-OCT-2000 (first entry)
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XX
KW Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.

XX
PF 25-FEB-2000: 200SEP-0301439.
XX
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 29-OCT-1999; 99US-0162142.

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  Ratio: 5.091          Gaps: 0
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34 alGluserArgIleIleLeuSerProCysValGlnAlaThrAsnArgIy 50
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208 TGGATCTTGGATTAATTCCTGCTCCGTGTGTACAGCGACGAATCGCGT 257
51 GlyIleValAlaIaArgAsnSerAlaGlyAlaSerGluThrSerValAla 67
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258 GGAATGTGCGCGAATAATTCACGAGAGCGTCGAGACAGATGTTAT 307
67 eValaArgArgArgAspSerProProValGluGluGluIncysGlnIleGlu 84
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308 AGTACGACGCGGAGATTCCTCCGTTGAAGACAGATGCAAAATCGAAG 357
84 lUglAspSerSerValSerCysSerThrSerGluGluIuysSerIys 100
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358 AAGAGATTCGTCGCTTCGTTGTTCTTCTACATCGGAAGAGAAATCGAAA 407
101 ArgArgIleGluPheValAspLeuGluGluAsnAsnGlyAspAspArgGl 117
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408 CGAGAAATCGAATTTGTAGATCTTGAGGAAATAACGGTACGATCGTGA 457
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456 AACAGAAACGTCGTGATTTACGATGATTTGAATAGACTGAGATCA 507
134 eAsnMetAspSerSerSerValAlaValAlaGluAspValGluSerArgArg 150
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556 AGGTAAAGGAAAGATCTCCATGAGACGGTGAAGAACTGAGTTAGAGA 607
167 pPhehGluValAlaGluLysAspLeuArgAsnLysLeuLeuGluGlyS 184
608 TTTTTCAGGTGGCGAGAAAGATCTTCGAATAGATTGTTGGAATGTT 657
184 eMetLysTyrAsnPhaSpPheGluLysAspGluProLeuGluGlyGly 200
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seq_documentation_block:
ID AAX25015 standard; CDNA; 932 BP.

AC AAX25015;

DF 05-JUL-1999 (first entry)

DE Arabidopsis cyclin-dependent kinase inhibitor FL39 cDNA clone.

XX Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI;

KW FL39; plant development; transgenic plant; cell cycle;

KW growth regulator; herbicide; ds.

XX Arabidopsis thaliana.

OS Key Location/Qualifiers

FT CDS 86..715

FT polyA_signal 915..920

FT misc_feature 305..932

FT /tag- C

FT /note- "this region of the sequence is specifically

FT claimed in Claim 1(c)"

FT MO9914331-A2.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-EP05895.

XX 24-DEC-1997; 97EP-020411.

XX 16-SEP-1997; 97EP-0202838.

XX (CROP-) CROPESTIGN NV.

XX De Almeida J, De Veylder L, Inze D, Landrieu I;

XX WPI: 1999-229535/19.

XX P-PSDB: AAM98179.

XX DNA encoding inhibitor of cyclin-dependent kinase

XX Claim 1b; Page 72-74; 88pp; English.

XX This is the DNA sequence of FL39, a cDNA clone that encodes a new
CC cyclin-dependent kinase (CDK) inhibitor (see AAM98179) of Arabidopsis
CC thaliana. New plant products with a putative CDK inhibitory
CC function were screened by using a two-hybrid system with CDC2aa1
CC protein as bait and a library made from an RNA mixture of A.
CC thaliana cell suspensions harvested at the early exponential,
CC exponential, early stationary and stationary phases. Positive
CC clones LDV39, LDV66 and LDV15 were obtained. Clone FL39 was
CC isolated from a flower cDNA library using partial clone LDV39 as
CC probe. Clone FL66 (see AAX25015) was similarly obtained using LDV66.
CC Another CDK inhibitor, ALPCDK1 (see AAX25018), was obtained from
CC alfalfa. Results established that several CDK inhibitors exist
CC in plants and that these inhibitors are expressed at different
CC time points and may have different functions during the development
CC of the plant. CDK inhibitors, nucleic acids, antibodies, promoter
CC sequences, related recombinant DNA and vectors are all useful: for
CC diagnosis (no details); for modulating the cycle, division and/or
CC growth of plant cells; for altering activity of CDK; for modulating
CC growth inhibition in plants caused by environmental stress; for
CC inducing male or female sterility; for altering cell division
CC progression in plants, bacteria, fungi, insect and animal cells;
CC and to screen for agonists or antagonists that are potentially
CC useful as growth regulators or herbicides. Plants of any sort can
CC be treated, e.g. to alter their size or resistance to disease.
XX
Sequence 932 BP; 289 A; 125 C; 254 G; 264 T; 0 other:

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Quality: 1064.00 Length: 209

Ratio: 5.091 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-574-735c-2 x AAX25015

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34 aGluSerArgIleIleLeuSerProCysValGlnAlaThrAsnArgGly 50

186 TCGAATCTAGCATTAATTCGTCTCCCTGCTGTACAGCGACGAAATCCGCT 235

51 GlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValAla 67

236 GGAATTTGGCGAGAAATTCACGAGAGCGTCGAGACGAGTGTGTAT 285

67 eValArgArgArgAspSerProProValGluGluGlnCysGlnIleGluG 84

286 AGTACGACGCGGAGATTCCTCCGGTTGAAGAACGTGTCAATGGAAG 335

84 LuGluAspSerSerValSerCysCysSerThrSerGluGluLysSerLys 100

336 AAGAGATTCGTCGCTGTTGCTGTTGTTCTACATCGAAGAAATCGAAG 385

101 ArgArgIleGluPheValAspLeuGluGluAsnAsnGlyAspAspArg 117

386 CGAGAAATCGAATTTGTAGATCTTGAGAAATTAACGGTACGATCGTGA 435

117 uthrglutThrSertPrIleTyrAspAspLeuansnlyssSerGluGluSerM 134

436 AACAGAAACGTCGTGATTTACGATGATTTGAATAGACTGAGATCA 485

134 eAsnMetAspSerSerSerValAlaValAlaGluAspValGluSerArgArg 150

486 TGACATGATCTCTTCCTCGGTGGCTGTGAAGATAGAGTCTGCCGC 535
 151 ArgLeuArgLysSerLeuHisGluThrValLysGluAlaGluLeuGluAs 167
 536 AGGTTAAGGAAGAGTCTCCATGAGACGGTGAAGGAACTGATTGAAGA 585
 167 pPhePheGlnValAlaGluLysAspLeuArgAsnLysLeuLeuGluCys 184
 586 TTTTTCAGGTGGCGGAGAAAGATCTCGGAAATAGTTGTTGCAATTT 635
 184 erMetLysTyrAsnPheAspPheGluLysAspGluProLeuGluGly 200
 636 CTATGAAGTATTAACCTTCGATTTCGAAAGATGAGCCACTTGTTGAGAGA 685
 201 ArgTyrGluTyrPValLysLeuAsnPro 209
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seq_documentation_block:
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 XX AAC85204;
 AC
 XX 22-MAR-2001 (first entry)
 DT
 XX Plant D-like cyclin inhibitor BRO3 coding sequence.
 DE
 XX Plant: D-like cyclin inhibitor gene; BRO4, hyperplastic; variant;
 KM growth rate; dividing cells; inactivation; protoplast; seed;
 KW root cell; meristem; leaf; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT CDS 69..620
 FT /tag= a
 FT /product= BRO3
 PN WO200069883-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 15-MAY-2000; 2000WO-US13379.
 XX
 PR 14-MAY-1999; 99US-0134373.
 XX
 PA (HUTC-) HUTCHINSON CANCER RES CENT ERD.
 XX
 PI Roberts J, Kelly B;
 XX
 DR WPI; 2001-024998/03.
 XX
 DR P-PSDB; AAB47004.
 XX
 PT Functionally inactivating expression of plant D-like cyclin inhibitor
 XX gene for producing a hyperplastic variant plant, modulating the growth
 XX and/or yield of plants, and increasing the proportion of dividing cells
 XX
 PS Example 1; Page 39-40; 50pp; English.
 XX

The sequence given in AAC85204 represents a plant D1 cyclin inhibitor gene, BRO3. This sequence was isolated using a yeast two hybrid screen. The BRO3 protein was found to contain a seven amino acid sequence cyclin binding domain similar to that of BRO1, BRO2 and BRO4 (See also AAB47005-6). This sequence is homologous to a sequence present in a D-like cyclin inhibitor gene and when integrated at the corresponding locus, functionally inactivates plant D-like cyclin inhibitor protein expression. The BRO4 coding sequence may be used to produce a hyperplastic variant plant, increase the growth rate of a plant, or increase the proportion of dividing cells in a plant cell population, relative to a wild-type plant, by functionally inactivating the expression of a plant D-like cyclin inhibitor

CC gene in a plant. BRO4 is useful for increasing the proportion of
 CC dividing cells in a plant cell population comprising protoplast,
 CC seeds, root cells, meristem cells or leaf cells.
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 XX Sequence 809 BP; 268 A; 110 C; 213 G; 218 T; 0 other;

alignment_scores:
 Quality: 1027.00 Length: 201
 Ratio: 5.109 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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 42 roCysValGlnAlaThrAsnArgGlyIleValAlaArgAsnSerAla 58
 115 CGTGTGACAGCGACGACATCGCGTGAATTTGGCGAGAAATTCAGCA 164
 59 GlyAlaSerGluThrSerValValIleValArgArgArgAspSerPro 75
 165 GGACGTCGCGAGACGAGTGTATAGTACGACGCGAGATCTCTCC 214
 75 oValGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 92
 215 GGTGGAAGAACAGTCAATCGAAGAGAGATTCCTCGGTTTCGCTT 264
 92 YsSerThrSerGluGluLysSerLysArgArgIleGluPheValAspLeu 108
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XX 16-DEC-1999.
XX
XX 08-JUN-1999; 99MO-CA00532.
XX
XX 08-JUN-1998; 98CA-2235978.
XX
XX 31-DEC-1998; 98CA-2256121.
XX
XX (MIAC ) AGRIC & AGRIFOOD CANADA.
XX (UTSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX (CANA ) NAT RES COUNCIL CANADA.
XX
XX Wang H, Fowke LC, Crosby WL;
XX
XX WPI: 2000-097540/08.
XX
XX P-PSDB; AAY44335.
XX
XX
XX Modifying plant cell development using nucleic acid encoding inhibitor
XX of cyclin-dependent kinase, or corresponding antisense sequence, e.g.
XX for inducing male sterility -
XX
XX Claim 5; Fig 1; 58pp; English.
XX
XX
XX The present sequence is a cDNA encoding A. thaliana Cyclin-Dependent
XX kinase (CDK) inhibitor, ICK1. Interactor of Cdc2 kinase 1 (ICK1)
XX interacts with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3. Growth,
XX morphogenesis, multiplication, enlargement, differentiation and
XX maturation of plant cells can be modified by transforming them with
XX nucleic acid encoding CDK inhibitor or antisense construct complementary
XX to the inhibitor gene, operably linked to a tissue-specific promoter.
XX The transgenic plants exhibit alteration of traits such as petals, male
XX sterility and ability to set seeds.
XX
XX
XX Sequence 904 BP; 307 A; 107 C; 229 G; 261 T; 0 other;
XX
XX

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alignment_scores:

Quality: 209.00 Length: 195
 Ratio: 1.917 Gaps: 9
 Percent Similarity: 55.897 Percent Identity: 34.359

alignment_block:

US-09-574-735c-2 x AA229415 ..

Align seg 1/1 to: AA229415 from: 1 to: 904

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82 GGAATTGTA.....GAAGCTGAGACTTCGTCAACGATATATGCACCT 122
   .....SerValIleValAlaArgArgAspSerProProValG 77
   :|||
   :|||
123 ACGGAGCCGCGAATGTTATGTTAGATCGGAAAAATCAAGCTCTGCT 172
   l u g l u g l n c y s g l n l e g l u g l u a s p s e r s e r v a l s e r c y s s e r 93
   :|:
   :|:
173 CC.....GTGCTCGGTATATGATGATTCATGCTCTTGTAGTGA 213
   T h e r s e r g l u g l u l y s e r l y s a r g a r g l l e g l u p h e v a l a s p l e u g l u 110
   :|:
   :|:
214 AGCATGATGATTAAGAGAAA.....GAATTAATACATCTGAGAGA 254

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111 :|||||
112 :|||||
255 GGAAGAT...AAGATGCTGACACTGAAACGTCGACGTATCGACGGGTA 301
124 .....TyrAspAspleu 127
302 CGAAGAGAACCTTTTGAATAATCTGAGAGAGAGAGAGAAAGAAATTA 351
128 AsnlySerGluUserMetAsnMetAspSerSerValAlaValG1 144
129 :|||||
130 :|||||
352 AGTAATCCATGAGAAATTTATTCATCGCAATTTGATCGGGGTTAAAGA 401
144 uaspaValUserArgrArgrArgrArgrArgrArgrArgrArgrArgr 160
145 :|||||
146 :|||||
402 ATCGTTAGATTGTTGTTGACCGGAGGAGAAACGATGAGAGACGGTGA 451
161 .....LysGlu 162
452 CGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501
163 AlagluLeugluAspPheGluValAlaValAlaValAspleuArgrAsnly 179
164 :|||||
165 :|||||
502 TCGGAATGGAAGATTTTGTGGAAGCTGAGAAACACTCAAGAGAA 551
179 sLeuLeugluCysSerMetLysTyrAsnPheAspPheGluLysAspGlu 196
180 :|||||
181 :|||||
552 ATTC.....AAGAAGAGTACAAATTCGATTTTCAGAGAGAGAGAG 592
196 roleuGlyGlyArgrTyrGluTrpValLysLeu 207
197 :|||||
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593 CATTA...GAAGGACGTTACGATGGGTAAAGTTA 624
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seq_documentation_block:
ID AAZ29418 standard; cDNA; 642 BP.

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XX AC AAZ29418;
XX AC
XX DT 29-FEB-2000 (first entry)
XX DE Arabidopsis thaliana CDK inhibitor, ICN6 encoding cDNA.
XX DE
XX KM Cyclin-dependent kinase inhibitor; CDK; Interactor of Cyclin 6;
XX KM ICN6; Cdc2; D-class cyclin; CycD1; CycD3; morphogenesis;
XX KM antisense construct; tissue-specific promoter; transgenic plant;
XX KM male sterility; ds.
XX OS
XX FH Unidentified.
XX FH
XX FT Key Location/Qualifiers
XX FT CDS 1..624
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XX FT /product="ICN6"
XX PN W09964599-A1.
XX PD 16-DEC-1999.
XX PE 08-JUN-1999; 99WO-CA00532.
XX PR 08-JUN-1998; 98CA-2235978.
XX PR 31-DEC-1998; 98CA-2256121.
XX PA (MIAC) AGRIC & AGRIFOOD CANADA.
XX PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX PA (CANADA) NAT RES COUNCIL CANADA.
XX PI Wang H, Fowke LC, Crosby WL;
XX PI
XX WPI: 2000-097540/08.
XX DR P-PSDB: AAY44338.
XX

```

```

PT Modifying plant cell development using nucleic acid encoding inhibitor
PT of cyclin-dependent kinase, or corresponding antisense sequence, e.g.
PT for inducing male sterility -
XX
XX PS Disclosure; Fig 5; 58pp; English.
XX
XX CC The present sequence is a cDNA encoding ICN6 which inhibits A. thaliana
XX CC Cyclin-dependent kinase (CDK). Interactor of Cyclin 6 (ICN6)
XX CC interacts with Cdc2a, D-class cyclins, CycD1, CycD2 and
XX CC shares functional and sequence similarity with ICK1. Growth,
XX CC morphogenesis, multiplication, enlargement, differentiation and
XX CC maturation of plant cells can be modified by transforming them with
XX CC nucleic acid encoding CDK inhibitor or antisense construct complementary
XX CC to the inhibitor gene, operably linked to a tissue-specific promoter.
XX CC The transgenic plants exhibit alteration of traits such as petals, male
XX CC sterility and ability to set seeds.
SQ Sequence 642 BP; 211 A; 140 C; 152 G; 139 T; 0 other;

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alignment_scores:
Quality: 182.50 Length: 205
Ratio: 1.508 Gaps: 9
Percent Similarity: 59.024 Percent Identity: 27.805

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alignment_block:
US-09-574-735c-2 x AAZ29418

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Align seg 1/1 to: AAZ29418 from: 1 to: 642

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21 :|||||
22 :|||||
79 TCACACATCAAGAGAGATGACGATGATGATGATGATGATGATGATGATG 128
36 rArgIleIleuSerProCysValAlaValAlaValAsnArgrGlyIleVal 53
37 :|||||
38 :|||||
129 A..... 129
53 AlAlaArgrAsnSerAlaGlyAlaSerGluTrpSerValAlaValAlaVal 69
54 :|||||
55 :|||||
130 .CGGAGAGACACTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 177
70 ArgrArgrAspSerProValGluGluGluGluGluGluGluGluGluGlu 86
71 :|||||
72 :|||||
178 GTTTCAGATTCGCGAGGTTCTGCTCGCTGCTGCTGCTGCTGCTGCTGCT 227
86 P.....SerSerValSer.....CysCysSerThrSerGlu 97
87 :|||||
88 :|||||
228 CGATCATCTAAGCTCAAGCAATCAAGCTCTGTTGTTCCAGAGAGAACTA 277
97 LysSerLysArgrArgrIleGluPheValAspleuGluGluGluGluGlu 113
98 :|||||
99 :|||||
278 ACGAATACGCTACTCGCTCTCTCAATTTCAAGATCGAGGCTCAT..... 321
114 AspAspArgrGluTrpGluTrpSerTrpIleTyrAspAsp..... 126
115 :|||||
116 :|||||
322 GAATCTCCGAAACCGAAATCTCAAGCTTCAAGCAATTTTCAGAGAA 371
127 .....LeuAsnLysSerGlu.....GluSerMetAsnMetAsp 138
128 :|||||
129 :|||||
372 ACAGGCAATTTCAATCAAGCGAATCTGGAGAAACGAGAAATGAGACT 421
138 erSerSerValAlaValAlaGluAspValGluSerArgrArgrArgrArgr 154
139 :|||||
140 :|||||
422 CGGCGAGAGAGAGATGAGAGAT...CAGAGAAACGAGAGAGAGAGAG 468
155 SerLeuHisGluTrpValLysGluAlaGluGluGluGluGluGluGluGlu 171
156 :|||||
157 :|||||
469 AAGATGAAATAATCACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 518
171 lAlaGluLysAspleuArgrAsnLysLeuGluGluGluGluGluGluGluGlu 188
172 :|||||
173 :|||||
519 GCGGAGAGATACGAACGAAACGATTCACAGAA.....AAGTTA 559

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PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
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PR 20-AUG-1999; 99US-0149929.

PR 23-AUG-1999; 99US-0149902.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
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PR 13-OCT-1999; 99US-0159293.
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PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161359.
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PR 29-OCT-1999; 99US-0162142.

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Percent Similarity: 60.544 Percent Identity: 38.095

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US-09-574-735c-2 x AAC36219 ..

Align seg 1/1 to: AAC36219 from: 1 to: 585

70 ArgArgAspSerProPValGluGluGlnCysGlnIleGluGluGluAs 86
||||:||||| ||||:||||| :
81 AGCGACAGATAGT.....AAGATCACTGTTCTTAACGATGCTCTCA 121
86 pSerSerValSerCysCysSerTherSerGluGlu.Lys..... 98
::: |||::||| ::||| ::||| :
122 AGATCATGTACATGCTGAGAAACAGACGACGACGATCATGATCAGG 171

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99 .....SerLysArgArgIleGluPheValAspLeuGluGluAsnAsnG1 113
117 CCTCTCTCAAGATGATTCAGATTCTGATTCATGCACGAACACGCG 221
113 yAspAspArgGluThrGluThrSerTrpIleTyraSpAspLeuAsnLys 130
222 TTACATTGGTGGTTGAG.....TATGTGCATGACCCACAGAT 259
130 eRGluGluSerMetAsnMetAspSerSerSerValAlaValGluAspVal 146
260 CTGGCAGATCGTC.....GTT 276
147 GluSerArgArgArgLeuArgLysSerLeuHisGluThrValGluAla 163
277 GAATTGAACGGAAGGTTGAACAAAGT.....CG 305
163 aGluLeuGluAspPhePheGluValAlaGluLysAspLeuArgAsnLysL 180
306 TGTATTCAGCCACGTTTGGATGTTGGTGTCAAGAAATTGAAG..... 350
180 euLeuGluCysSerMetLysTyraSpAspPheGluLysAspGluPro 196
351 ..TTGGAAATGTTCTATGAAGTAACTTCGATTCGAGAAAGATGAGCCA 398
197 LeuGlyGlyArgTyrGluThrValLysLeuAsnPro 209
399 CTGGGTGAGGAAGATACGAGTGGTTAAATTGAATCCA 437

seq_name: /SIDS2/gcgdata/geneseq/NA2000.DAT:AAA95288
seq_documentation_block:
ID AAA95288 standard; cDNA; 1116 BP.
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AC AAA95288;
XX
DT 17-JAN-2001 (first entry)
XX
XX Soybean cyclin-dependent kinase inhibitor coding sequence #3.
KM Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
OS CKI; cell growth; herbicide; ss.
XX Glycine max.
FH Key Location/Qualifiers
FT CDS 143..760
FT /*tag= a
FT /*product= "CDKI"
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PN W0200060087-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000MO-US09106.
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PR 07-APR-1999; 99US-0128192.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Klein TM, Weng Z, Cahoon RE;
XX
DR WPI: 2000-679375/66.
DR P-PSDB: AAB27254.
XX
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
PT herbicides and plant growth inhibitors
XX
XX Claim 2; Page 49-50; 58pp; English.
XX
CC The present sequence is the coding sequence for the soybean
CC cyclin-dependent kinase inhibitor (CDKI). It was isolated by searching a
CC soybean pod cDNA library for sequences similar to those encoding the

```

```

CC CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis
CC thaliana. CDKI is involved in the cell cycle, and may promote or inhibit
CC cell division and growth. The coding sequence and the protein it encodes
CC are useful in the production of transgenic plants which produce increased
CC or decreased amounts of the CDKI protein, in the identification of
CC herbicides, in genetic and physical mapping and in the isolation of the
CC CDKI gene in other organisms.
XX
SQ Sequence 1116 BP; 339 A; 236 C; 269 G; 272 T; 0 other:

alignment_scores:
Quality: 161.50 Length: 222
Ratio: 1.196 Gaps: 11
Percent Similarity: 60.811 Percent Identity: 27.027

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US-09-574-735C-2 x AAA95288 ..

Align seg 1/1 to: AAA95288 from: 1 to: 1116

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20 r.....ThrValLysArgArgLysMetGluGluGluValAspLeuValG 35
211 TGAACCATCATCCAAAGAAAGAAAGATGACGAAACATCTACTAAC..... 253
35 LuserArgIleIleLeuSerProCysValGlnAlaThrAsnArgGlyGly 51
254 .....CAAGAGCCAAACCTCCAAAGCTCCGAGA..... 283
52 IleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValIleVal 68
284 .....ACGAGTTCCTCCCTCCGTCACAAACGACGACGTCGAGAGAT 327
68 LArgArgArgAspSerProProValGluGluGlnGlyGlnGluGluG 85
328 GGTTCAGCCGCTGTCGCGGAGATGGTTCAGCAACCTCCGAGGCCCA 377
85 LuAspSerSerVal.....SerCysCysSerThr.....SerGluGlu 97
378 CCTCCAGTGAATTCGCGGCTCTGCTGCTCCAGACGAGATCCATGGC 427
98 LysSerLysArgArgIleGluPheValAspLeuGluGlu..... 110
428 CTCGATCAGACAGAGATCAACGCTTAGATCTGAGGTGAGAGCGCGCA 477
111 .....AsnAsnGlyAspAspArgGluThrGluThrS 121
478 AGTGAACAGTCGACGTCGCAATGTTGTCATGAATTTGAGAGAGA.... 523
121 eRTripIleTyraSpAspLeuAsnLysSerGluGluSerMetAsp 137
524 .....GAGATGAACGTTCCAGCGAG...CTGCGCGAGAT 556
138 SerSerSerValAlaValGluAspValGluSerArgArgArgLeuArgly 154
557 TCTCAGAGACCGGAGCCCAATGGATCAATTCACCGTGTTCATCAA 606
154 sSerLeuHisGluThrValLysGluAlaGluLeuGluAspPhePheGlu 171
607 GGCA..AAGCCATCCCTACCGCAATTGAGCTCGAGAAATTCCTGCGTG 653
171 AlaGluLysAspLeuArgAsnLysLeuLeuGluCysSerMetLysTy 187
654 CCTCGAGAAAGACATTCAGAAACGATTCACAGAC.....ACATAC 694
188 AsnPheAspPheGluLysAspGluProLeuGlyGlyArgTyrGluThr 204
695 AATTATGATATTTGTTAAAGACGATACCGCTG...GAAGACGCTACGAGTG 741

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204 pvallylsleuansPro 209
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 742 GGTTCAGTTGAGCCT 757

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT.AAA95287

seq_documentation_block:

ID AAA95287 standard; cDNA; 620 BP.

AC AAA95287;

DT 17-JAN-2001 (first entry)

DE Soybean cyclin-dependent kinase inhibitor coding sequence #2.

XX Soybean: cyclin-dependent kinase inhibitor; cell cycle; cell division;

KW CDK1; cell growth; herbicide; ss.

XX glycine max.

OS Key Location/Qualifiers

FT CDS 1..264

FT /tag- a

FT /product- "CDK1"

PN MO200060087-A2.

PD 12-OCT-2000.

PF 06-APR-2000; 2000MO-0509106.

PR 07-APR-1999; 99US-0128192.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Klein TM, Weng Z, Cahoon RE;

DR WPI; 2000-679375/66.

PT Cyclin dependent kinase inhibitor sequences, useful for identifying

PT herbicides and plant growth inhibitors

PS Claim 2; Page 49; 58pp; English.

XX The present sequence is the coding sequence for the soybean

CC cyclin-dependent kinase inhibitor (CDK1). It was isolated by searching a

CC soybean seedling cDNA library for sequences similar to those encoding the

CC CDK1 from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis

CC thaliana. CDK1 is involved in the cell cycle, and may promote or inhibit

CC cell division and growth. The coding sequence and the protein it encodes

CC are useful in the production of transgenic plants which produce increased

CC or decreased amounts of the CDK1 protein, in the identification of the

CC herbicides, in genetic and physical mapping and in the isolation of the

CC CDK1 gene in other organisms.

SQ Sequence 620 BP; 191 A; 111 C; 134 G; 183 T; 1 other;

alignment_scores:

Quality: 138.50 Length: 81

Ratio: 2.388 Gaps: 3

Percent Similarity: 71.605 Percent Identity: 40.741

alignment_block:

US-09-574-735C-2 x AAA95287 ..

Align seg 1/1 to: AAA95287 from: 1 to: 620

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34 AAAAGTTCCAGCGAGCTTCGAGAGATTTCACGAGCCGAGCCATGGA 83

145 pvalGluSerArgArgLeuArgGlySerLeuHisGluThrVallysg 162
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 84 GATCAATTCTCACCGCTGCTTATCAAGGCA...AAAGCCATGCCCTACCG 130
 162 LuAlaGluLeuGluAspPhePheGluValAlaGluLysAspLeuArgAsn 178
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 131 AGTTGAGCTCGAGGAATCTCTGCTGCGGAGAAAGACATTCAGAA 180
 179 LysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspG1 195
 181 CGATTTCAAGAC.....AAGTACATATTATGATATTGTTAAGACGT 221
 195 uProLeuGlyGlyGlyArgTyrGluTyrPvalLysLeuansPro 209
 222 ACCACTG...GAAGRCGCTACGAGTGCGTTCACTGTAAGCCA 261

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

1 (bases 1 to 754)
 Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town,C.D., Van Aken,S., Uteback,T., Cho,J. and Fraser,C.M.
 ESTs from one month old nitrogen-fixing root nodules of Medicago truncatula, 2001

JOURNAL
 Unpublished (2001)
 Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
 Tel: 612 625 5715
 Fax: 651-649-5058
 Email: vance004@maroon.tc.umn.edu
 University of Minnesota name: M382960e TIGR sequence name: MTC00777K More information is available at: http://www.medicago.org
 Seq primer: Skmod (CTA gAA CTA gTg gAT CC).

FEATURES
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 /cultivar="genotype A17"
 /db_xref="taxon:3880"
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 /dev_stage="effective root nodules harvested one month post inoculation with Sinorhizobium meliloti"
 /lab_host="E. coli strain XL0R"
 /note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from StrataGene and packaged using GigaPack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XL0R cells."

BASE COUNT
 210 a 189 c 159 g 196 t

ORIGIN

alignment_scores:
 Quality: 131.00 Length: 223
 Ratio: 1.129 Gaps: 12
 Percent Similarity: 52.018 Percent Identity: 28.251

alignment_block:
 US-09-574-735c-2 x BG581898 ..

Align seg 1/1 to: BG581898 from: 1 to: 754

5 ArgAArgGluArgAspValValGluGluAsnGlyValThrThrTh 21
 |||||
 84 CGAGCTGCCGCCCGGAT.....AATGAATCACCACATCTCACT 121
 21 TVallysrArg.....LysMetGluGluIuv 31
 |||||
 122 CCACCGCGCTGCTCGGACAGCTGCCAAACCTCGCACTCCAGAA 171
 31 AlaAspGluValGluSerArg.....IleIleLeuSerProCysValGln 45
 |||||
 172 TCTCC...GCCGAATCACCTGATTCCTTCCTTCCTCGACGTCGCG 218
 46 AlaThrAsnArgGlyGlyIleValAlaArgAsnSerAlaGlyAlaSerG 62
 |||||
 219 CCGCGCGCTCGTAAGTTCCTCGCGCCCTTCACACTCGCAAGAGACG 268
 62 urhSerValValIleValArg.ArgArgAspSerProValGluGlu 78
 |||||
 269 GTTCTCCCGGAATAATCCAGCCTCTG..... 294

79 GlnCysGlnIleGluGluGluAspSerSerValSerCysSerThrSe 95
 ::|||
 295 GAATGTCGGTGAAGAA.....TTGGAAATTTCTGTGCTGA 332
 95 rGluGluYSerSerLysArgArgIleGluPheVal..... 106
 |||||
 333 AGAAGAGAAATGAGATCGATGCGATTCGCTGTGAGGTTCTTTTG 382
 107AspLeuGluGluAsnGlyAspAspArgGluThrGluThrSer 121
 ::|||
 383 GTGAATAATTCGACAGATGATGCTAGACATAGAACACTAGCGAAGC 432
 122 TrpIleYrAspAspLeuAsnLysSerGluGluSerMetAsnMetAspSe 138
 ::|||
 433ACACCTTGTAAGTTAAATCAGGATTC 458
 138 rSerSerValAlaValGluAspValGluSerArgArgLeuArgLys 155
 ||||
 459 AAGTGTCTATTCATACCCCTGCTCAACCAAGCAAGCAAGCAACCA 508
 155 erLeuHisGlu.....ThrValLysGluAlaGluLeuGlu 166
 ::|||
 509 TTATTCAGAAACACATGCAGAAATACTCCACAACTAAATGAAGTGAT 558
 167 AspPhePheGluValAlaGluLysAspLeuArgAsnLysLeuLeuGluCy 183
 ::|||
 559 GAATTCCTTGCCCTTGCGACAGACGACACGACATTTATTTATGAA.. 606
 183 sSerMetLysTrpAsnAspPheGluLysAspLeuProLeuGlyGly 200
 |||||
 607AAGTACATTTTGAATGATGAATGATGATGATGATGATGAT 646
 200 LysArgTyrGluTrpVal 205
 |||||
 647 GACGCTACGAATGGCTC 663

seq_name: gb_est2:BG581898

seq_documentation_block:
 LOCUS BG581898 766 bp mRNA EST 11-APR-2001
 DEFINITION EST483735 GVN Medicago truncatula cDNA clone pgVN-66M24 5' end,
 mRNA sequence.
 ACCESSION BG581898
 VERSION BG581898.1 GI:13597062
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.

REFERENCE
 1 (bases 1 to 766)
 Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town,C.D., Van Aken,S., Uteback,T., Cho,J. and Fraser,C.M.
 ESTs from one month old nitrogen-fixing root nodules of Medicago truncatula, 2001

JOURNAL
 Unpublished (2001)
 Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
 Tel: 612 625 5715
 Fax: 651-649-5058
 Email: vance004@maroon.tc.umn.edu
 University of Minnesota name: M383061e TIGR sequence name: MTC08847K More information is available at: http://www.medicago.org
 Seq primer: Skmod (CTA gAA CTA gTg gAT CC).

FEATURES
 source
 1..766
 /organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"

```

/clone="pgvn-66m24"
/clone_lib="GVN"
/tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells."

```

```

BASE COUNT      214 a      190 c      162 g      200 t
ORIGIN

```

```

alignment_scores:
    Quality: 131.00      Length: 223
    Ratio: 1.129        Gaps: 12
    Percent Similarity: 52.018      Percent Identity: 28.251

```

```

alignment_block:
US-09-574-735c-2 x BG581998 ..

```

```

Align seq 1/1 to: BG581998 from: 1 to: 766

```

```

5  ArgArGArGluArGAspValValGluGluAsnGlyValThrThrThr 21
   |||||
84 CGAGCTGCGCGCGCTGAT.....AATGAAATTCACCATCTCACT 121
   |||||
21 rVallyArGArG.....LysMetGluGluLuv 31
   |||||
122 CCACCGCGCTGCTCGGACAGTGCACAAACTCTCGCATCTCGAGAAA 171
   |||||
31 alaAspLeuValGluSerArg.....llelleuSerProCysValGln 45
   |||||
172 TCTCC...GCCGATTCACCTCGATCTCTCTCTCTCCAGCTCCGCGAG 218
   |||||
46 AlaThrAsnArGlglylleValAlaArGAsnSerAlaGlyAlaSerG 62
   |||||
219 CCGCGCGCTCGTAAAGTTCCTCGCGCTTCACCTCGCAAGAGAGCG 268
   |||||
62 urhSerValVallleValArg.ArGArGAspSerProProValGluGlu 78
   |||||
269 GTTCTCCGGAATAATCCAGGCTTCT..... 294
   |||||
79 GlnCysGlnlleGluGluAspSerSerValSerCysSerThrse 95
   |||||
295 GAATGTTGCTTGAGAAA.....TTGGGAATTTCTGTGCTGA 332
   |||||
95 rGluGluLysSerLysArGArGlleGluPheVal..... 106
   |||||
333 AGAAGAGATGAGATGCTGTATGCTGCTGTAAGGTTCTTTTG 382
   |||||
107 .....AspLeuGluGluAsnGlyAspAspArgGluThrGluThrSer 121
   |||||
383 GTGAAATTTGCGAGAGTGTATGATGATAGACATGACATGAGGAAGC 432
   |||||
122 TrpIleTyraSpAspLeuAsnLysSerGluGluSerMetAspSe 138
   |||||
433 .....ACACCTGTAGTTTAATCAGGAGATTC 458
   |||||
138 rSerSerValAlaValGluAspValGluSerArGArGleuArglyys 155
   |||||
459 AAGTCTCATTCATACCTGTGTTCAACCAAGCAAGAGCAACACA 508
   |||||
155 erLeuHisGlu.....ThrValLysGluAlaGluLendGlu 166
   |||||
509 TTATTCAGAAACACATGCAAGAAATTAATCAACTAATGAGTGGAT 558

```

```

167 AspPhePheGlnValAlaGluLysAspLeuArGAsnLysLeuLeuGluC 183
   |||||
559 GAATCTTTCCTTGCGACAGAGCAAGCAACAAAGCATTTATGGA... 606
   |||||
183 sSerMetLysTyraSpAspPheGlnLysAspGluPheLeuGlyG 200
   |||||
607 .....AAGTCAATTTTGTATGATGATGATGATGATGATGATGATG 646
   |||||
200 lYArGTYrGluTrpVal 205
   |||||
647 GACGTCACCAATGGGTC 663

```

```

seq_name: gb_est2:BG582049

```

```

seq_documentation_block: 785 bp mRNA EST 11-APR-2001
LOCUS BG582049
DEFINITION EST483787 GVN Medicago truncatula cDNA clone pgvn-66h11 5' end.

```

```

ACCESSION BG582049
VERSION BG582049.1 GI:13597113
KEYWORDS EST.
SOURCE
ORGANISM

```

```

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

```

```

REFERENCE 1 (bases 1 to 785)
AUTHORS Fedorova,M., Plesion,B.L., Samac,D.A., Vance,C.P., Gantl,G.S., Town
,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
TITLE ESTs from one month old nitrogen-fixing root nodules of Medicago
truncatula, 2001
JOURNAL Unpublished (2001)
COMMENT Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M38113e TIGR sequence name:
MTC0042TK More information is available at: http://www.medicago.org
Seq primer: Skmod (CTA gAA gTg gAT CC).

```

FEATURES

source

```

1. 785
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pgvn-66h11"
/clone_lib="GVN"
/tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells."

```

```

BASE COUNT      219 a      190 c      167 g      209 t
ORIGIN

```

```

alignment_scores:
    Quality: 131.00      Length: 223
    Ratio: 1.129        Gaps: 12
    Percent Similarity: 52.018      Percent Identity: 28.251

```

```

alignment_block:

```


Site-2: NotI. This cDNA library was constructed from mRNA isolated from hypocotyl and plumule tissues of seeds germinated for three days of the cultivar Williams.

Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and NotI. The cDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the pT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker.

BASE COUNT 170 a 158 c 145 g 147 t 3 others
ORIGIN

alignment_scores:
Quality: 114.00 Length: 126
Ratio: 1.629 Gaps: 6
Percent Similarity: 55.556 Percent Identity: 33.333

alignment_block:
US-09-574-735C-2 x BE347049 ..

Align seg 1/1 to: BE347049 from: 1 to: 623

```

87 SerSerValSerCysCysSerThrSerGluGluSerLysArgArgI1 103
||||| ||||||||| ||||| ||||| ||||| ||||| ||||| |||||
294 TCCGATCCCTCTGCTGCTGAGCTCCAGCCAGCTTACAGACCTCCACTCGT 343
103 egluPheValaspLeuGluGluAsnGlyAspAspArgGluThrGluT 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
344 GCCG...TCAGATCTGACAGACCAAGGTTTCGAACGGTAGAGACTCAA 390
120 hrSerTrpIleTyraaspLeuasn.....Lys 129
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
391 CCAGCCTCAATTCAATCGTTCAGTGTGAGTTCGAGCTTCCGAGAC 440
130 SerGluGluSer...MetAsnMetaspSerSerSerValAlaValGluAs 145
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
441 TCGAGGAGATCGCGCATGATTCGCGCGAAGTTCGCGCGCTGCTCGAN 490
145 pValGluSerArgArgLeuArgLysSerLeuHisGluThrValLysG 162
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
491 AGTG.....AGACGCCGCCGA 507
162 luAlaGluLeuGluaspPhePheGlnValAlaGluLysaspLeuArgAsn 178
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
508 AGCGCGAGATCGAAGAGTNTTCCGATGCGTGANAGTACGACGCAAAA 557
179 LysLeuLeuGluCysSerMetLysTyraaspPheaspPheGluLysaspG 195
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
558 CCGTTCACAGAG.....AAGTACAACTTGTGATTTGATGAGATTT 598
195 uProLeuGlyGlyArgTyrgluTIP 204
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
599 GCCGTTG...GAGGTCGCTACCACTGG 623

```

seq_name: gb_est2:BG841133

seq_documentation_block:

LOCUS BG841133 604 bp mRNA EST 29-MAY-2001
DEFINITION MEST18-A04.T3 ISUM4-TN zea mays cDNA clone MEST18-A04 3', mRNA

ACCESSION BG841133

VERSION BG841133.2 GI:14243442

SOURCE EST.

ORGANISM zea mays.

KEYWORDS zea mays.

REFERENCE Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

Clade: Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 604)

AUTHORS Qiu, F., Cui, F., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
TITLE Expressed Sequence Tags from B73 Maize Seedlings and Silks
JOURNAL Unpublished (2001)
COMMENT On May 25, 2001 this sequence version replaced gi:14207455.
Contact: Patrick S. Schnable

Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES
source

1..604
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST18-A04"
/clone_1lb="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5',
AACTGACAGATTCGCGCGCGCGAGATTTTCTTTTCTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelino Bento Soares (Genome
Research 6: 791-806, 1996)."

BASE COUNT 120 a 174 c 170 g 140 t
ORIGIN

alignment_scores:
Quality: 113.50 Length: 46
Ratio: 3.243 Gaps: 1
Percent Similarity: 76.087 Percent Identity: 43.478

alignment_block:
US-09-574-735C-2 x BG841133/rev ..

Align seg 1/1 to reverse of: BG841133 from: 1 to: 604

```

164 GluLeuGluaspPhePheGlnValAlaGluLysaspLeuArgAsnLysLe 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
405 GAGGTGGAGGCGGCTTCGCGCGACGCGGCGCATGCGCGCGCGCTT 356
180 uLeuLysSerMetLysTyraaspPheaspPheGluLysaspGluProL 197
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
355 C.....GGGTCAAGTACACTATGACCTGTCAGAGGCGCTCCCA 315
197 euGlyGlyArgTyrgluTIPValLysLeuAsnPro 209
::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
314 TGGACGGCGCGCGGTACAGTGGTCCGAGTGGCGGCC 277

```

seq_name: gb_est1:A1728644

seq_documentation_block:

LOCUS A1728644 646 bp mRNA EST 11-JUN-1999
DEFINITION BNUGH11291 Six-day cotton fiber Gossypium hirsutum cDNA 5' similar
to (AJ002173) cyclin-dependent kinase inhibitor protein
[Chenopodium rubrum], mRNA sequence.

ACCESSION A1728644

VERSION A1728644.1 GI:5047496

KEYWORDS EST.
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 646)
AUTHORS Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
TITLE ESTs from developing cotton fiber
JOURNAL Unpublished (1999)
COMMENT Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burrbnl@bnl.gov
Seq primer: T3 primer.
Location/Qualifiers
1. 646
/organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/note="Vector: pBluescript II KS+"

BASE COUNT 198 a 141 c 150 g 153 t 4 others
ORIGIN

alignment_scores:
Quality: 111.00 Length: 226
Ratio: 0.941 Gaps: 13
Percent Similarity: 52.212 Percent Identity: 25.221

alignment_block:
US-09-574-735c-2 x AT728644 ..

Align seg 1/1 to: AT728644 from: 1 to: 646

```

6  Argarglualrgaspsvalvalglulnslgualttrthr.... 20
   :|||||: :|||||: :|||||: :|||||: :|||||:
60  AACGCAAGTGCAGACGAGCTGAATGCAATGCAACGAGCTTCTC 109
   :|||||: :|||||: :|||||: :|||||: :|||||:
21  .....ThrvallysArArplysmetglu.... 29
   :|||||: :|||||: :|||||: :|||||: :|||||:
110 ATTATCAAGAGACAAAACCTGTTGCTTCGAGATTCGACGAATTAG 159
   :|||||: :|||||: :|||||: :|||||: :|||||:
30  .....Gluvalaspleuvalgluserargyllelleuser 41
   :|||||: :|||||: :|||||: :|||||: :|||||:
160 AGTTAACTTCACCGACATTCGTCGCAACCATCGCATCTTCGAA 209
   :|||||: :|||||: :|||||: :|||||: :|||||:
42  .....Procyvalglinalathrasnaagly.... Gly11 52
   :|||||: :|||||: :|||||: :|||||: :|||||:
210 TCGCTGAACCAACCTATTACTTACTTCTCGGCTTCCTTGAGAGT 259
   :|||||: :|||||: :|||||: :|||||: :|||||:
52  eValaIaargasnservalglvalasergluthrservalValleVala 69
   :|||||: :|||||: :|||||: :|||||: :|||||:
260 GCTTCCGGAGATATGTGTCGGT..... 284
   :|||||: :|||||: :|||||: :|||||: :|||||:
69  rGArGArGAspsrProvalglulnslgualttrthr.... 85
   :|||||: :|||||: :|||||: :|||||: :|||||:
285  .....CTCTTCGCGGC 296
   :|||||: :|||||: :|||||: :|||||: :|||||:
86  AppSerValserCysSerThrSerGlu.....GluLysSerly 100
   :|||||: :|||||: :|||||: :|||||: :|||||:
297 AATTCAATCGCTTCGCTTCGAGCAACGAGCTGTGATATTCTCAA 346
   :|||||: :|||||: :|||||: :|||||: :|||||:
100  sArGArGllleGlupheValaspleuGlulnslgualttrthr.... 117
   :|||||: :|||||: :|||||: :|||||: :|||||:
347 ACATAGCTTGAGATTCTAGATCTAGAGCGGAAGAGT.....TTTG 387

```

```

117  luthrcluthrserrtrpletyraspsleuAsnllys...Sergluln 132
   :|||||: :|||||: :|||||: :|||||: :|||||:
388  AACTCAAAATCTCA...ACGTGACCAACGCTCAACAAATTCAGTAGAGA 434
   :|||||: :|||||: :|||||: :|||||: :|||||:
133  SerMetasMetaspsrSerservalAlaValgluaservalgluserAr 149
   :|||||: :|||||: :|||||: :|||||: :|||||:
435  ACACCTCCCTTAAGCGCATTTGTGAGACTCGACGAATTCATCGCGC 484
   :|||||: :|||||: :|||||: :|||||: :|||||:
149  gArGArGleuArGlySerleuHISgluthrVallys..... 161
   :|||||: :|||||: :|||||: :|||||: :|||||:
485  TGAG.....AAAAACCTCCGCGCTCAACGACGAACCGCGAGATTC 528
   :|||||: :|||||: :|||||: :|||||: :|||||:
162  .....GluAlaGlueuGlualasphnephneGlnValAlaGlulysAspleu 176
   :|||||: :|||||: :|||||: :|||||: :|||||:
529  CGTGGCAGCTGATGATGACGAGAAATCTCTCGCTCGCAAAAAGTAGAG 578
   :|||||: :|||||: :|||||: :|||||: :|||||:
177  ArGAsnlysluenuGlucysSerMetlyTYrAspAspPheglulny 193
   :|||||: :|||||: :|||||: :|||||: :|||||:
579  CAAMAAGATTTCGGAG.....AAGTACNATTATGATATCTCTCA 619
   :|||||: :|||||: :|||||: :|||||: :|||||:
193  sAspGluproleuGlyGlyArGTYr 202
   :|||||: :|||||: :|||||: :|||||: :|||||:
620  GATGTGCTCTC...GACGCTGATAC 644
   :|||||: :|||||: :|||||: :|||||: :|||||:
seq_name: gb_est2:BG908519
seq_documentation_block:
LOCUS BG908519 691 bp mRNA EST 05-JUN-2001
DEFINITION Talr1169A02R Talr1 Triticum aestivum cDNA clone Talr1169A02 5',
mRNA sequence.
ACCESSION BG908519
VERSION BG908519.1 GI:14316195
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 691)
Cloutier, S., Dong, G. and Walsh, A.
Wheat functional genomics - Thatcher Lr1 cDNA library
Unpublished (2001)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Darke Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average inset size is >2.2 kb
Plate: 169 row: A column: 02
Seq primer: M13 Reverse.
Location/Qualifiers
1. 691
/organism="Triticum aestivum"
/cultivar="Thatcher Lr1"
/db_xref="taxon:4565"
/clone_lib="Talr1169A02"
/clone_lib="Talr1"
/tissue_type="leaf tissue"
/dev_stage="14 days old"
/lab_host="E. coli XL0LR"
/note="Vector: Lambda ZapII; mass excised in plasmid
vector pBK-CMV (Stratagene).; Site_1: EcoRI; Site_2: XhoI;
mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
inoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avr1."
BASE COUNT 141 a 216 c 231 g 103 t
ORIGIN

```

alignment_scores:

Quality: 110.50 Length: 206
Ratio: 1.005 Gaps: 8
Percent Similarity: 53.398 Percent Identity: 23.301

alignment_block:

US-09-574-735C-2 x BG908519 ..

Align seg 1/1 to: BG908519 from: 1 to: 691

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seq_name: gb_est2:BG428484

seq_documentation_block:

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mRNA sequence.
ACCESSION BG428484
VERSION BG428484.1 GI:13334990
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 1322)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cyabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM1351 row: 0 column: 24
High quality sequence stop: 230.
Location/Qualifiers

FEATURES

source

1. 1322
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDMR-LIB (Clontech); Site: 1;
SfiI (ggcgctatggcc); Site: 2; SfiI (ggcgctatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATATATGCG-3' and 3' adaptor sequence:
5'-ATTGAGAGCGCGAGCGCGCGCGCATATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH-MGC Library."

BASE COUNT 621 a 232 c 401 g 68 t
ORIGIN

alignment_scores:

Quality: 109.00 Length: 177
Ratio: 1.112 Gaps: 8
Percent Similarity: 55.367 Percent Identity: 25.989

alignment_block:

US-09-574-735C-2 x BG428484 ..

Align seg 1/1 to: BG428484 from: 1 to: 1322

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Aljan sed 1/1 to reverse of: BH139743 from: 1 to: 941

OM of: US-09-574-735c-2 to: Issued_Patents_NA:* out_format: pfs
 Date: Jan 30, 2002 1:20 PM

About: Results were produced by the Gencore software, version 4.5,
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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 -DB=Issued_Patents_NA -QWRT=fastap -SUFFIX=p2n.rn1
 -GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000
 -LOOPEXT=0.000 -OGAPOP=4.500 -OGAPEXT=0.000 -XGAPOP=10.000
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 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45 -DOCALLIGN=200
 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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Search information block:

Query: US-09-574-735c-2

Query length: 209

Database: Issued_Patents_NA:*

Database sequences: 351203

Search time (sec): 44.180000

score list:

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seq_documentation block:

Sequence 3, Application US/07667276A
 Patent No. 5470971
 GENERAL INFORMATION:
 APPLICANT: Kondo, Keiji
 TITLE OF INVENTION: Inouye, Masayori
 TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
 TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Weiser & Associates
 STREET: 230 S. Fifteenth Street, Suite 500
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/667,276A
 FILING DATE: 11-MAR-1991
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Weiser, Gerard J.
 REGISTRATION NUMBER: 19,763
 REFERENCE/DOCKET NUMBER: 377,5351P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-875-8383
 TELEFAX: 215-875-8394
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2017 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: Internal
 ORIGINAL SOURCE:
 ORGANISM: Saccharomyces cerevisiae
 STRAIN: S288C
 FEATURE:
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 FEATURE:
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 US-07-667-276A-3

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US-09-574-735c-2 x US-07-667-276A-3 ..

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seq documentation block:
; Sequence 5, Application US/08533306A
; Patent No. 5837457
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI

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; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/533,306A
; FILING DATE: September 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869COB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; INDIVIDUAL ISOLATE: Sample 2
; TISSUE TYPE: Acute myelomonocytic leukemia, M4b0
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 16[inv(16)(p13q22)]
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2451
; US-08-533-306A-5

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Align seg 1/1 to: US-08-533-306A-5 from: 1 to: 2680

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17 ValThrThrThrVallylsArgArglysmetglugluValaspLe 33
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961 GTRCCAACTCGAAGAAAGCAAGCAAGAAATTCATCAGTTG.....TT 1004
33 uValGluSerArgilleleuserProcyValglAlaThrsmArg 50
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1005 AGCCGAGAGAGAAACATCTCTCAATACCGGATGAGAGGAGCAGAG 1054
50 lylGlylileValAlaArgsmSerAlaGlyAlaSerGluThrSerVal 66
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1055 CTGAGCGCAAGCCAGGAG.....AAGGAACCAAGGCCCTG 1092
67 lileValArgArgAspSerProProValglugluInclncslnle 83
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1093 TCCCTGGCTCG.....GCCCTGAAAGAGGCTTGAAGCA 1130
83 uGluGluAspSerSerValSerCysSerThrSerGlu..... 96
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1131 AGAGAACTCGAGCGGACCAAAATGCTCAAGCCGAAATGGAAGCC 1180
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1264 .ATGAAGACGCGAGCTGGAAGAGCTGAGAGCAGCTGCAAGCCTCGAGAG 1312
132 Luser.....MetAsnMet..... 136
:|||||
1313 ACGCCAAACTCGCGCTGGAAGTCACATGACAGCGCTCAAGGCCAGTTC 1362
137 .....AspSerSerSerValAlaValGluAspValGluSerArgArg 151
||| :||| :|||||
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:||||| :||| :|||||
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168 hePheGluValAlaGluLysAspLeuArg.....Asn 178
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179 LysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspG 195
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1492 AAGAAAGCTGGAAGGGGACCTGAA...GACCTGAGCTTCAGCGGCACTC 1538
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1539 TGCCATC...AAGGGAGGAGAGAGCCATCAAG 1569
seq_name: /cgn2_6/ptodata/2/ina/5B.COMB.seq:US-08-742-923A-5
seq_documentation_block:
Sequence 5, Application US/08742923A
Patent No. 5869611
GENERAL INFORMATION:
APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,923A
FILING DATE: No. 5869611ember 1, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-00869DVC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
TELEFAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2680 base pairs
type: nucleic acid

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? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? INDIVIDUAL ISOLATE: Sample 2
? TISSUE TYPE: Acute myelomonocytic leukemia, M4e0
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT: 16(inv(16)(p13q22))
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..2451
? US-08-742-923A-5

alignment_scores:
Quality: 100.50 Length: 228
Ratio: 0.838 Gaps: 13
Percent Similarity: 52.632 Percent Identity: 25.439

alignment_block:
US-09-574-735C-2 x US-08-742-923A-5 ..
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17 ValThrThrThrValLysArgLysMetGluGluValAspLe 33
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961 GTGTCAACCTGGAAGAGAGAGAGAAATTTGATCAGTTC.....TT 1004
33 uValGluSerArgIleIleLeuSerProCysValGlnAlaThrAsnArgG 50
|:||||| :||| :|||
1005 AGCCGAGAGAAACATCTCTTCCAAATACCGGATGAGGACGAGAG 1054
50 lGlylIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValVal 66
:|:||||| :||||| :|||||
1055 CTGAGGACAGAACCCAGGAG.....AAGCAACCAAGCCCTCG 1092
67 lIleValArgArgArgAspSerProProValGluGluGlnCysGlnIleG 83
:|:||||| :||| :|||
1093 TCCTTGCGCTCG.....GCCCTTGAAGAGGCTTGGAGCCCA 1130
83 uGluGluAspSerSerValSerCysSerThrSerGlu..... 96
:||||| :||| :|||
1131 AGAGAACTCGAGCGGACCAACAAATGCTCAAGCCGAATGGAAGACC 1180
97 .....GluLys 98
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1181 TGCTACGCTCCAAAGATGACGTGGCCCAAGACCTCCATGAGCTGAGAG 1230
99 SerLysArgArgIleGluPheValAspLeuGluGluAsnGlyAspAs 115
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115 pArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnLysSerGluG 132
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1264 .ATGAAGACGCGAGCTGGAAGAGCTGAGAGCAGCTGCAAGCCTCGAGAG 1312
132 Luser.....MetAsnMet..... 136
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1313 ACGCCAAACTCGCGCTGGAAGTCACATGACAGCGCTCAAGGCCAGTTC 1362
137 .....AspSerSerSerValAlaValGluAspValGluSerArgArg 151
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1363 GAAAGGATCTCCAAAGCCCGGAGCAGCAGATGAGAGAGAGAGAGCA 1412
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seq_name: /cgn2_6/ptodata/2/lna/5B_COMB.seq:US-08-533-306A-3

seq_documentation_block:
; Sequence 3, Application US/08533306A
; Patent No. 5837457
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; TITLE OF INVENTION: Rearrangements
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/533,306A
; FILING DATE: September 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869COB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2887 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; INDIVIDUAL ISOLATE: Sample 1
; TISSUE TYPE: Acute myelomonocytic leukemia, M4E0
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 16[inv(16)(p13q22)]
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2658
; US-08-533-306A-3

alignment_scores:
Quality: 100.50 Length: 228
Ratio: 0.838 Gaps: 13
Percent Similarity: 52.632 Percent Identity: 25.439

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33 uValGluSerArgLleIleLeuSerProCysValGluAlaThrAsnArg 50
1212 AGCCGAGAGAGAAAACATCTTCCAAATATACGCGGATGAGAGGACAGAG 1261
50 LgcGlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValAl 66
1262 CTGAGCGAGAACCCAGGAG.....AAGGAACCAAGCCCTG 1299
67 IleValArgArgArgAspSerProProValGluGluCysGlnIleG1 83
1300 TCCTGCTCGG.....GCCCTGAAAGAGGCTTGGAAACCA 1337
83 uGluGluAspSerSerValSerCysSerThrSerGlu..... 96
1338 AGAGAACTGAGCGGACCAACAATGCTCAAAAGCCGAATGGAAGACC 1387
97 .....GluLys 98
1388 TGTCTAGCTCCAAAGATGACGTGGGCAAGAACGTCATGAGCTGGAGAG 1437
99 SerLysArgArgLleGluPheValAspLeuGluGluAsnAsnGlyAspAs 115
1438 TCCAAGCGGCGCTGAG...ACCCAGATGAGGAG..... 1470
115 PargGluThrGluThrSerTrpLleTyrAspAspLeuAsnLysSerGlu 132
1471 ATGAAGACGACGTGGAGAGCTGGAGAGAGCTGCACCTCGGAGG 1519
132 Luser.....MetAsnMet..... 136
1520 ACGCCAAACTCGGCGTGAAGTCAACATGACAGCGGCTCAAGGCCAGATTG 1569
137 .....AspSerSerSerValAlaValGluAspValGluSerArgArg 151
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151 GLeuArgLysSerLeuHisGluThrValLysGluAlaGluLeuGluAsp 168
1620 ACTCAGAGACAGCTTCACGAG.....TATGAGACGAGACTGGAAGAC 1662
168 hePheGlnValAlaGluLysAspLeuArg.....Asn 178
1663 .....GAGCGAAACGACAGCTGCCCTGGCAGCTGCAGCAAG 1698
179 LysLeuLeuGluCysSerMetLysTyrAsnPhaSpheGluLysAspG1 195
1699 AAGAAAGCTGGAAGGAGGACCTGAAA...GACCTGGAGCTTCAGGCCGACTC 1745
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seq_documentation_block:
; Sequence 3, Application US/08742923A
; Patent No. 5869611
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16

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? TITLE OF INVENTION: Rearrangements
? NUMBER OF SEQUENCES: 14
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Hainess, Dickey & Pierce, P.L.C.
? STREET: P.O. Box 828
? CITY: Bloomfield Hills
? STATE: MI
? COUNTRY: USA
? ZIP: 48303
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/742,923A
? FILING DATE: No. 5869611ember 1, 1996
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, Dean F.
? REGISTRATION NUMBER: 36683
? REFERENCE/DOCKET NUMBER: 2115-00869DVC
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (810) 641-1600
? TELEFAX: (810) 641-0270
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2887 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? INDIVIDUAL ISOLATE: Sample 1
? TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT: 16(inv(16)(p13q22))
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..2658
? US-08-742-923A-3

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  Quality: 100.50      Length: 228
  Ratio: 0.838        Gaps: 13
  Percent Similarity: 52.632   Percent Identity: 25.439

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33 uvalgluserargileleleuserProcysvalglinalatrrasnarg 50
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  ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1262 CTGAGGAGCAAGCAAGCAGAG.....AAGGAACCAAGGCCCTG 1299
67 llevalargargargasperProvalagluginlncysglInleel 83
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97 .....glutys 98
1388 TGGTCAGCTCCAAGATGACGTGGCAAGACGTCATGAGCTGGAAG 1437
99 SerlysrargarglleglupheValaspleuglugluasnarglyaspas 115
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1438 TCCAAAGCGGCGCTGGAG...ACCGAGATGAGAGG..... 1470
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1471 .ATGAAGACGACGCTGGAAGAGACTGAGAGCAGCTGCAGAGCTCGAG 1519
132 luser.....Metasmet..... 136
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168 hepheglvalalaglulysaspLeuarg.....Asn 178
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1663 .....GAGCAAGCAAGACGTGCCCTGACAGCTGCAGCAAG 1698
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seq_documentation_block:
  Sequence 5, Application US/09214564A
  Patent No. 6150515
  GENERAL INFORMATION:
  APPLICANT: Sharp, Phillip A.
  TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
  FILE REFERENCE: M0656/7042 Elongation By HIV-1 TAT
  CURRENT APPLICATION NUMBER: US/09/214,564A
  PRIOR FILING DATE: 1999-08-18
  PRIOR APPLICATION NUMBER: US 60/021,218
  PRIOR FILING DATE: 1996-07-03
  PRIOR APPLICATION NUMBER: US 60/033,152
  PRIOR FILING DATE: 1996-12-13
  PRIOR APPLICATION NUMBER: PCT/US97/11713
  PRIOR FILING DATE: 1997-07-03
  NUMBER OF SEQ ID NOS: 5
  SOFTWARE: FastSeq for Windows Version 3.0
  SEQ ID NO 5
  LENGTH: 2672
  TYPE: DNA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: 58..2319
  US-09-214-564A-5

alignment_scores:
  Quality: 100.00      Length: 211

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Ratio: 0.971 Gaps: 12
Percent Similarity: 48.815 Percent Identity: 26.066

alignment block:

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Align seg 1/1 to: US-09-214-564A-5 from: 1 to: 2672

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44 LglAlaThrAsnArgGlyIleValAlaArgAsnSerAlaGlyAlas 61
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1348 .GAAAGACAGAGATGCGGGA.....GAATTGAAAGAGAGTCTT 1387
61 ergIuThrSerValIleValAlaArgArgAspSerProValGlu 77
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1388 CTGAAACAAATGCT.....AAGGAAAGTACCCCGAAGAAAGAG 1425
78 GluGluCysGlnIleGluGluAspSerSerValSerCys..... 91
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1426 GCTGAAGAGAGCTGCCCTGAAAGAAATCTGAAGAGGCTGCCCAAG 1475
92 .....CysSerThrSerGlu..... 96
1476 AGGGTTGAAGCAGCTGCTCCCAAGAGCTGAAGAGCAATCCG 1525
97 .....GluysSerLysArgArgIle 103
1526 TAAGAGATCTGAAGAGATAGTCTTAAGAGAGCTTAAGAGAGACA 1575
104 GluPheValAspLeuGluAsnArgIleValAlaArgAsnSerAlaGly 120
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1576 CTCAAAATATGTTGTGAAG..AATGCCCTTCAAGAGATCTGA.. 1620
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seq_name: /cgn2_6/ptdata/2/lna/6A.COMB.seq:US-09-214-564A-1
seq_documentation_block:
; Sequence 1, Application US/09214564A
; Patent No. 6150515
; GENERAL INFORMATION:
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Zhou, Qiang
; TITLE OF INVENTION: RAT-SF: Cofactor For Stimulation Of Transcriptional
; TITLE OF INVENTION: Elongation By HIV-1 TAT
; FILE REFERENCE: M0656/7042
; CURRENT APPLICATION NUMBER: US/09/214,564A
; CURRENT FILING DATE: 1999-08-18

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; PRIOR APPLICATION NUMBER: US 60/021,218
; PRIOR FILING DATE: 1996-07-03
; PRIOR APPLICATION NUMBER: US 60/033,152
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: PCT/US97/11713
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2815
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..2371
; NAME/KEY: unsure
; LOCATION: 46..46
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: unsure
; LOCATION: 2731..2731
; OTHER INFORMATION: n = a, c, g or t
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alignment_scores: Quality: 100.00 Length: 211
Ratio: 0.971 Gaps: 12
Percent Similarity: 48.815 Percent Identity: 26.066

alignment block:

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Align seg 1/1 to: US-09-214-564A-1 from: 1 to: 2815

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1528 AGGGTTGAAGCAGCTGCTCCCAAGAGCTCTGAAGAGCAATCCG 1577
97 .....GluysSerLysArgArgIle 103
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104 GluPheValAspLeuGluAsnArgIleValAlaArgAsnSerAlaGly 120
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120 rSerTrpIleTyrAspAspLeuAsnLys..... 129
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1673 .....GATGACCTCAACAGAGAGTCTGAAGAGAGGTTGGCC 1709
130 ..SerGluGluSerMetAspSerSerSerValAlaValGluAsp 145
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1710 CCAGAAAGAGTCCGAGAGAGATCTCAGAGAAAGAGTGTGATGAAGAC 1759
146 ValGluSerArgArgArg..... 151
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152 ...LeuArglySerLeuHisGluThrValIleGluAlaGluLeuGlu 167
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 167 spphephegluValAlaGluIleGluAspLeuArgAsnLysLeuLeuGluLys 183
 1860 AA.....AATGTTCTTGACAAAGAGTTAGAGAAATGACTCTGA... 1900
 184 SerMetLysTyrAsnPhespphegluLysAsp 194
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seq_name: /cgn2_6/ptodata/2/ina/6a_COMB.seq:US-08-374-077C-1

seq_documentation_block:
 ; Sequence 1, Application US/08374077C
 ; Patent No. 6027912
 ; GENERAL INFORMATION:
 ; APPLICANT: Hall, Linda M.
 ; APPLICANT: Ren, Dejian
 ; APPLICANT: Zheng, Wei
 ; APPLICANT: Dubald, Manuel Marcel Paul
 ; TITLE OF INVENTION: Genes Encoding an Invertebrate Alpha
 ; TITLE OF INVENTION: Calcium Channel Subunit
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314-3187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/374,077C
 ; FILING DATE: 19-JAN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McGowan, Malcolm M.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 022650-264
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8075 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 157..7704
 ; US-08-374-077C-1

alignment_scores:
 Quality: 98.00 Length: 208
 Ratio: 0.891 Gaps: 8
 Percent Similarity: 52.885 Percent Identity: 17.788

alignment_block:
 US-09-574-735C-2 x US-08-374-077C-1 ..
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 1217 TCCGATATATTCAGAT.....TGCTGGCGGGCGAAC 1248
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 64 rValValIleValArgArg.....ArgAspSerProValGluGlu 79
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 79 IncysGlnIleGluGluLysAspSerSerValSerCysCysSerThrSer 95
 1340 CATGCGAGATTAACGAGGAGGAC..... 1362
 96 GluGluLysSerLysArgArgIleGluPheValAspLeuGluIleAsn 112
 1363GACGACGAGACGAGAGA 1379
 112 nGlyAspArgArgGluThrGluThrSerTrpIleTyrAspLeuAsn 129
 1380 CGCGGAC.....TACGGTATTTGATC 1402
 129 YsserGluGluSerMetAsn.....MetAspSerSerValAla 142
 1403 GGGAGATCAAGAGCTAGACGACGAGAGCCCGAGGGACCACTTAC 1452
 143 ValGluAspValGluSerArgArgArgLeuArgLysSerLeuHisGlu 159
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 159 rValIleGluAlaGluLeuGluAspPhephegluValAlaGluLysAsp 176
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 193 LysAspGluProLeuGlyGly 200
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seq_name: /cgn2_6/ptodata/2/ina/6b_COMB.seq:US-08-895-590-1

seq_documentation_block:
 ; Sequence 1, Application US/08895590
 ; Patent No. 6207410
 ; GENERAL INFORMATION:
 ; APPLICANT: Hall, Linda M.
 ; APPLICANT: Ren, Dejian
 ; APPLICANT: Zheng, Wei
 ; APPLICANT: Dubald, Manuel Marcel Paul
 ; TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314-3187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

Percent Similarity: 54.955 Percent Identity: 20.270


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seq_name: /cgn2-0/prodata/47/ma/35_COMB.seq:US-08-905-445-1
seq_documentation_block:
: Sequence 7, Application US/08905445
: Patient No. 5864015
GENERAL INFORMATION:
APPLICANT: Pfeundschuh, Michael
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: felfe & Lynch
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1 MetAlaIleValArgArgGluArgSpValValGluGluAsnGlyVa 17
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1193 CTGGAGGCCATCAGGTCCAAACTGGCAACGAAGAAGCACGCATCTCGT 1242
17 lnhTrThrThrValLysArgArgLysMetCluGlulValAlaspLeuV 34
   :::: :::: :::: |||:::|| |:::
1243 AGAATAATGAGAAGCAGCTTAACAATAATTACAGCAAGCTCAATAATTAAGCTTAA 1292
34 aIGluserArgIleIleuSerProCysValGlnAlaIleThr..... 47
   ||| :::::|||| :::: |||
1293 AGSAGCTNAGGTACTCTGCAGCAACCAATTCMAATGAACCAACCAGTTATT 1342
48 .....AsnAr 49
1343 GATTAATTTTACATCACAGCTCAAGGCTACTCGAAGAAAAGCTCTTGGAACCT 1392
49 gGIgLyIleValAlaArgasnSerAlaGlyAlaSerGluThrSerValV 66
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1393 TGAATGACCTCGGAAGAAGCATGTTCCGAAGGTAAATCGGAATGAAGAAAC 1442
66 alIleValArgArgArgspSerProprovalGluGluGln..... 79
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96 uGluSerSerIysArgArgIleGluPheValAspLeuGluGluAsnAng 113
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1534 AGAGCTCCAGGGAGAGAGCTAAAGCTTACCTACCTCAGGAAAAAT 1579
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113 LysAspArgGluThrGluThrSerThrPleIytrAspAspLeuAsnLys 129
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seq documentation block:
; Sequence 67, Application US/08235836C
; Patent No. 6248362
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
; TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET:
; CITY: Upton
; STATE: NY
; COUNTRY: USA
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,836C
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,191
; FILING DATE: 01-11-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret C.
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: BNL93-28A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 282-7338
; TELEFAX: (516) 282-3729
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2081 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2081
; US-08-235-836C-67

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  Percent Similarity: 49.091 Percent Identity: 21.364

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22 LysArgArgLysMetGluGluGluValAspLeuValGluSerArgIleI 39
   ::::: ::::: ::::: :::::
966 TGTTAGAGAGAGAGATTCACAGAGATATGACGAGATTAAATGAAGAA 1011
   ::::: ::::: ::::: :::::
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1012 .....AAG 1014
56 AsnSerAlaGlyAlaSerGluThrSerValValIleValArgArgArg 72
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1015 AATTGGCCAAACCTGGTGATGTAAGT.....AAG 1041
72 PserProProValGluGluGluCysGlnIleGluGlu.....GluAsp 87
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104 GluPheValAspLeuGluGluAsnAsnGlyAspAspArgGluThrGlu 120
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137 sPserSerSerValAlaValGluAspValGluSerArgArgArgIleArg 153
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154 LysSerLeuHisGluThrValLysGlu.....AlaG1 164
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178 AsnLysLeuGluGluCysSerMetLysTyrAsnPheAspPheGluLys 194
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1408 GAGAGAGTAATGAATTTGCAAGCTTAACACACATAGATGATGTAATC 1457
194 pGluProLeu 197

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APPLICANT: Jon D. Kratochvil
APPLICANT: Eric Russell
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the Urinary
FILE REFERENCE: 6180, US, 01
CURRENT APPLICATION NUMBER: US/09/153, 804
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
US-09-153-804-8

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Quality: 94.00 Length: 213
Ratio: 0.879 Gaps: 11
Percent Similarity: 50.235 Percent Identity: 22.535

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40 userProcysValGlnAlaThrAsnArgGlyIleValAlaArgAsn 57
751 ..... 751

57 eraLagIyAlaSerGluThrSerValAla.....ValArg 69
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752 .....TCGACACATCTGTGCTGCTGCATGCACAAAGCCGC 790
70 ArgArgAspSerProValGluGluGlnCysGlnIleGluGluAs 86
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791 TCCCTGGACATGAGACATCATTCGTGAGTCAGGACAGCAGACGAGA 840
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841 T.....ATTGCCAACCGCAGCCGGCTGAGCTGAGACATGACCA 884
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seq_documentation_block:
Sequence 2, Application US/08973462B
Patent No. 6191270
GENERAL INFORMATION:
APPLICANT: DROULHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 5361
TYPE: DNA
ORGANISM: P. falciparum
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(5361)
US-08-973-462-2

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Percent Similarity: 51.659 Percent Identity: 24.171

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	LOCUS			
	DEFINITION	C.rubrum mRNA for cyclin-D like protein.	PLN	19-JUN-1997
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	VERSION	V10162.1	GI:1770189	
	KEYWORDS	cyclD gene; cyclin-D like protein.		
	SOURCE	red goosefoot.		
	ORGANISM	Chenopodium rubrum		
	REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	AUTHORS	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;		
	TITLE	Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.		
	JOURNAL	1 (bases 1 to 1699)		
	REFERENCE	Renz, A.		
	AUTHORS	Direct Submission		
	TITLE	Submitted (18-DEC-1996) A. Renz, Lehrstuhl fuer		
	JOURNAL	Pflanzenphysiologie, Universitaet Bayreuth, Universitaetsstr. 30,		
		95447 Bayreuth, FRG		
		2 (bases 1 to 1699)		
		Renz, A., Fountain, M. and Beck, E.		
		Nucleotide sequence of a cDNA encoding a D-type cyclin from a		
		photoautotrophic cell suspension culture of Chenopodium rubrum L.		
		Plant Physiol. In press		
		Location/Qualifiers		
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		LSLAARDENVPLILDVOSESKFEPAKIQEMRELVSTLRKMOSVTFEIDG		
		FIVSDGDKMSKLFOALIOIILITSGIGSLDMEPRSEIAVAASVTOTOOLVEFTTE		
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BASE COUNT	554	a	283	c 308 g 552 t others
ORIGIN				

Query Match	27.9%	Score 258.2	DB 8	Length 1699
Best Local Similarity	64.0%	Pred. NO. 2.5e-54		
Matches 440; Conservative	0;	Mismatches 238;	Indels 9;	Gaps 3;

[illegible]

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Qy	303	AGCAATGACACTTGGATGATCTTATTCGGTTCATGATTGCTTAAGTGGCAAGTGT	362
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BASE COUNT	A85077	A85077	1846 bp	DNA
ORIGIN	LOCUS	Sequence	21 from Patent WO9842851.	
	DEFINITION	A85077		
	ACCESSION	A85077.1	GI:6733818	
	VERSION			
	KEYWORDS	'Zea mays.'		
	SOURCE	Zea mays		
	ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Panicoideae; Panicoidae; Andropogoneae; Zea.		
REFERENCE	TITLE	Murray,J.A.		
AUTHORS	JOURNAL	PLANTS WITH MODIFIED GROWTH		
		Patent: WO 9842851-A 21 01-OCT-1998;		
		MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)		
FEATURES	source	Location/Qualifiers		
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Query Match	20.9%	Score 193.4;	DB 6;	Length 1846;
Best Local Similarity	59.8%;	Pred. NO. 4.4e-38;		
Matches 364;	Conservative 0;	Mismatches 236;	Indels 9;	Gaps 2;

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